

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:17:40 ; Search time 69 Seconds

(without alignments)

570.496 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGTSPFDSQSASRNKWSY.....LIIMKNASEKEKKRRN 248

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688.5	54.1	213	22	Testis Enhanced Ge
2	499.5	39.3	140	22	Testis Enhanced Ge
3	498.5	39.2	138	21	Arabidopsis thalia
4	498.5	39.2	154	21	Arabidopsis thalia
5	495	38.9	110	21	Arabidopsis thalia
6	492.5	38.7	129	21	Arabidopsis thalia
7	491.5	38.6	236	22	Arabidopsis thalia
8	483.5	38.0	255	21	Rovine mammary tis
9	477.5	37.5	237	19	Lung cancer associ
					Bax inhibitor BI-1

10	331.5	26.1	245	23	ABP42996
11	324	25.5	277	22	AAU30218
12	312	24.5	245	22	ABB63069
13	192	15.1	305	22	ABB57985
14	172	13.5	341	22	ABB58798
15	171	13.4	346	21	AAAG49311
16	166	13.1	122	21	AAAG03753
17	165	13.0	242	22	AAAB64490
18	165	13.0	345	20	AAW81998
19	165	13.0	345	21	AAW79139
20	165	13.0	345	21	AAW66631
21	165	13.0	345	21	AAW59435
22	165	13.0	345	22	AAAB65154
23	165	13.0	345	23	ABP61812
24	165	13.0	345	23	ABG34030
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26	165	13.0	345	24	ABP71505
27	165	13.0	345	24	ABU59047
28	165	13.0	345	24	ABU59194
29	165	13.0	345	24	ABU59343
30	165	13.0	345	24	ABU60478
31	165	13.0	345	24	ABU57969
32	165	13.0	345	24	ABU58900
33	165	13.0	345	24	ABU13860
34	165	13.0	345	24	ABU10815
35	165	13.0	346	19	AAW74901
36	165	13.0	346	23	ABG95353
37	165	13.0	351	20	AAW76620
38	165	13.0	351	21	AAAB43975
39	143.5	11.3	250	22	AAAB4489
40	132	10.4	319	21	AAW83263
41	128.5	10.1	241	20	AAW37315
42	123	9.7	290	21	AAW33365
43	123	9.7	324	22	ABG60180
44	121	9.5	227	24	ABP77220
45	118.5	9.3	221	21	AAW33367

ALIGNMENTS

RESULT 1

AAAB65755

ID AAB65755 standard; Protein; 213 AA.

XX AAB65755;

XX

XX 27-MAR-2001 (first entry)

XX Testis Enhanced Gene Transcript protein #1.

XX Cell death modulator; programmed cell death; apoptosis;

XX forestry plant.

XX Pinus radiata.

XX WO200075331-A1.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-NZ00086.

XX 04-JUN-1999; 99US-0325932.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Flinn B, Lasham A;

XX WPI; 2001-061724/07.

XX N-PSDB; AAF44782.

XX Novel defender against cell death polynucleotide useful for modulating

PT programmed cell death pathway and specific development pathways in
PT forestry plant -

XX Claim 22; Pages 81-82; 142pp; English.

XX The present invention relates to coding sequences (see AAF44740-F44840
CC and AAF4843-F44844) and proteins (see AAB65714-B65814) involved in
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins
CC of the present invention are useful for modulating a PCD or cell death
CC pathway and various developmental pathways in a forestry plant, by
CC stably incorporating one of the present coding sequences into the genome
CC of the forestry plant, where the coding sequence provides a PCD pathway
CC that is not present in a native form of the forestry plant.

XX SQ Sequence 213 AA;

Query Match 54.1%; Score 688.5; DB 22; Length 213;
Best Local Similarity 64.6%; Pred. No. 3.9e-73;
Matches 137; Conservative 31; Mismatches 41; Indels 3; Gaps 2;

QY 39 QVYLTLCCALVSAAGAYLHILWNIGLLTMACMGSMVWLLSAP--PQEQKRVALLMA 96
Db 1 RVLUSCALVTAAGVYLHLLNLNIGLLTGLACIGSVIGLLSVPTSSNNEGKRAALLA 60
QY 97 AALFEGASIGPLIELGINFDPSPVFGAFVGCFAAAMLARRELYLGLSSG 156
Db 61 AAFKATGLPLIDAVINDSSILVAFVGTSLAFACFSAATARRRELYLGLGSG 120
QY 157 VSLFLWHPASSIFGSGMAVFKFELYFGLLVFVGYIVFDTPQETIEKALHGDMDYVKHALT 216
Db 121 ISILMLQLASSIFGSGSAIYTFEIVFGLLVFLGYIIFDQMIIEKADHGSDYDLKHSLD 180
QY 217 LFTDFGAVFVRIILIMKNA-SEKEKKKKRR 247
Db 181 LFTDFVAVFVRLVMIAKNADSKSREGKKRR 212

RESULT 2
AAB65756
ID AAB65756 standard; Protein; 140 AA.
XX AAB65756;
AC XX
DT 27-MAR-2001 (first entry)
XX
DE Testis Enhanced Gene Transcript protein #2.
XX
KW Cell death modulator; programmed cell death; PCD; apoptosis;
KW forestry plant.
XX
OS Pinus radiata.
XX
PN WO200075331-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-NZ00086.
XX
PR 04-JUN-1999; 99US-0325932.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Flinn B, Lasham A;
XX
DR WPI; 2001-061724/07.
DR N-PSDB; AAF44783.
XX
XX Novel defender against cell death polynucleotide useful for modulating
PT programmed cell death pathway and specific development pathways in
PT forestry plant -
XX
PS Claim 22; Page 82; 142pp; English.

XX The present invention relates to coding sequences (see AAF44740-F44840
CC and AAF4843-F44844) and proteins (see AAB65714-B65814) involved in
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins
CC of the present invention are useful for modulating a PCD or cell death
CC pathway and various developmental pathways in a forestry plant, by
CC stably incorporating one of the present coding sequences into the genome
CC of the forestry plant, where the coding sequence provides a PCD pathway
CC that is not present in a native form of the forestry plant.

XX SQ Sequence 140 AA;

Query Match 39.3%; Score 499.5; DB 22; Length 140;
Best Local Similarity 66.2%; Pred. No. 6.2e-51;
Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;

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Db 1 MDAFASLFQS---SGKWSHSDSLKNFRQISPAVQSHLKNVYLSLCCALMASAGAYLHLM 57
QY 61 WNTGGLLTTMACMGSMVWLLSAPPYQOKRVALLMAALFEGASIGPLIELGINFDPSPV 120
Db 58 LNTGGLLTTIACIGSVIWLISIPPHBEQKRFGLMAAALFEGACIGPLIEAALKVDPSPV 117
QY 121 FGAFCVCAVVGCFSAAMLARRELYLGG 151
Db 118 ISAFVGSALAFACFSGAA-----CWLGG 140

RESULT 3
AAG19970
ID AAG19970 standard; Protein; 138 AA.
XX AAG19970;
AC XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21975.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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Query Match 39.2%; Score 498.5; DB 21; Length 138;

Best Local Similarity 70.5%; Pred. No. Be-51;

Matches 91; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

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DB 1 MDAFSFDSQPGSRS-WSYDSLKNFRQISPAVQNHKRVYLTCCALVASAGAYLHL 59

QY 61 WNIGGLTTMACGSMVWLLSAPPYQEQKRKRVALLMAALFEAGSIGPLTIEIGINFDPSIV 120

DB 60 WNIGGILITIGCTGTMWLLSCPPYEHQKRLSLFASAVLEGASVGLIKVAIDVDPSTL 119

QY 121 FGAFFGCAV 129

DB 120 ITAFVGTAI 128

RESULT 4

AAAG19969
ID AAG19969 standard; Protein; 154 AA.

XX AAG19969;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 21974.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

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PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

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XX termination sequence.
OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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AC AAG54829;
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XX 18-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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XX Arabidopsis thaliana.
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PR 26-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 38.7%; Score 492.5; DB 21; Length 129;
Best local similarity 71.4%; Pred. No. 3.8e-50;
Matches 90; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 1 MEGTFFDSSASRNWSYDSLKFNFRQISPLIVQTHLKQVYILCCALVASAGAYLHIL 60
Db 1 MDAFFSFFDSQPGSRS-WSYDSLKFNFRQISPAVQNHVKRYLTCCALVASAFAYLHVL 59
QY 61 WNIGGLTTMACMGSMVLLSAPPYQOQKRVALLMAALFEGASIGPLIELGINFDPISV 120
Db 60 WNIGGLTTTGICIGTMIWLLSCPPYEHQKRLSLLFASVLEGSVGLIKVAIDVDPISL 119
QY 121 FGAFVG 126
Db 120 ITAFVG 125

RESULT 7
AAB87615
ID AAB87615 standard; protein; 236 AA.
XX AC AAB87615;
XX DT 15-MAY-2001 (first entry)
XX DE Bovine mammary tissue derived protein #6.
XX DE Bovine; mammary gland; cancer; tumour; angiogenesis.
XX KW Bos taurus.
XX OS WO200114553-A1.
XX PN 01-MAR-2001.
XX PD 23-AUG-2000; 2000WO-NZ00166.
XX PF 23-AUG-1999; 99US-0150330.
XX PR (GENE-) GENESIS RES & DEV CORP LTD.
XX PA (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
XX PI Havukkala LJ, Gleen M, Grigor MR, Molenaar AJ;
XX WPI; 2001-226619/23.
XX New polypeptides and polynucleotides encoding the polypeptides, which
XX are expressed in bovine mammary gland tissue, useful for stimulating
XX mammary gland growth or function, or inducing differentiation of milk
XX producing cells -
XX Claim 11; Page 62; 97pp; English.
XX The present invention relates to proteins derived from bovine
XX mammary gland cells. The invention is useful for stimulating
XX bovine mammary gland cell growth and function, inhibiting the
XX growth of various mammary gland cancer cells, inhibiting
XX angiogenesis and vascularization of tumours, or modulating
XX the growth of blood vessels in a mammal.
XX Sequence 236 AA;

```


Db 71 FIQAGLLSALGSLIMILWLMATPHSHETEQKRIGLGLAGFAFLQVGVGLPALEFCIAVNPS 130
 QY 119 IVFGAFVGCNAVFGCFSAAMLAARRREYLYLGGLLSGVSLLEWLHFPASSIFGGSMAVFK 178
 Db 131 ILPTAFMGTAIETCFETLSALYARRRSYFLGGILMSSPELGAFASLGNGFF-GSIWLFQ 189
 QY 179 FELYGGLLVFVGYIVFTDQRIEKAHL 205
 Db 190 ANLYXGLVVMCGFAFLILSLKRPNM 216

RESULT 11

AAU30218

ID AAU30218 standard; Protein; 277 AA.

XX AC AAU30218;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #709.

XX KW Human; vaccination; gene therapy; nutritional supplement;

XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WC200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US08656.

XX PR 18-APR-2000; 2000US-0552929.

XX PR 26-JAN-2001; 2001US-0770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic

XX PT vaccination, testing and therapy -

XX PS Claim 20; Page 262; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The

XX CC polypeptides and antibodies to the polypeptides are useful for

XX CC determining the presence of or predisposition to a disease associated

XX CC with altered levels of polypeptide. The polypeptides are also useful for

XX CC identifying agents (agonists and antagonists) that bind to them. Cells

XX CC expressing the proteins are useful for identifying a therapeutic agent

XX CC for use in treatment of a pathology related to aberrant expression or

XX CC physiological interactions of the polypeptide. Vectors comprising

XX CC the nucleic acids encoding the polypeptides and cells genetically

XX CC engineered to express them are also useful for producing the proteins.

XX CC The proteins are useful in genetic vaccination, testing and

XX CC therapy, and can be used as nutritional supplements. They may be used to

XX CC increase stem cell proliferation; to regulate haematopoiesis; and in

XX CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;

XX CC immune suppression and/or stimulation; as anti-inflammatory agents; and

XX CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid

XX CC sequences of novel human secreted proteins of the invention.

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Db 17 GTMIFD-----RKITFDALLKFSHUTPTQOAHMKVYASFPALCYFGAAAGAYVNMVT 70
 QY 62 NI--GGLLTTMACSGMVWLLSAPPYQ--FQKRV--ALLMAALFEGASIGPLI---ELG 112
 Db 71 HFTQAGLLSALGSLITLIMILWLMATPHSHETEQKRIGLGLAGFAFLQVGVGLPALEFCIAVNPS 130
 QY 113 INFDPISIVFGAFVGCNAVFGCFSAAMLAARRREYLYLGGLLSGVSLLEWLHFPASSIFGGSMAVFK 178
 Db 131 VQRQASLP-TAEWGHSGNSFPATLSALLCRRPSPSYFLGGILMSSPELGAFASLGNGFF-GSIWLFQ 189
 QY 179 FELYGGLLVFVGYIVFTDQRIEKAHL 205
 Db 190 ANLYXGLVVMCGFAFLILSLKRPNM 216

RESULT 12

ABB63069

ID ABB63069 standard; Protein; 245 AA.

XX AC ABB63069;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 15999.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WC200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.

XX PR 23-MAR-2000; 2000US-191637P.

XX PR 11-JUL-2000; 2000US-0614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers BW;

XX DR WPI; 2001-656860/75.

XX N-PSDB; ABL071172.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more

XX PT genes from Drosophila and for elucidating cell signalling and cell-cell

XX PT interactions -

XX PS Disclosure; SEQ ID NO 15999; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent

XX CC capable of detecting 1000 or more genes from Drosophila. The invention is

XX CC useful in developmental biology and in elucidating cell signalling and

XX CC cell-cell interactions in higher eukaryotes for the development of

XX CC insecticides, therapeutics and pharmaceutical drugs. The invention

XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

XX CC sequences (ABL01840-ABL16175) and the encoded proteins

XX CC (ABB57737-ABB72072).

XX CC The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequences.

XX CC

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Query Match

Best Local Similarity 24.5%; Score 312; DB 22; Length 245;

Matches 77; Conservative 48; Mismatches 83; Indels 16; Gaps 5;

QY 31 PLVQTHLKQVYLTCCALVASAAGAYLHI--LNNIGGLITTTMACM-----GSMVWLLSAPP 88
 Db 25 PYVREHLSKVMYVLTGTAATAAMGMLQMRDLDLG---VLAAVATLVVLGLHFYKDD 80
 QY 89 -----KRVALLMAALFEFASIGPLIEIGLNFDPSTVFGAFVGCACVFGCFSAAMLARR 143
 Db 81 GKNYYTRGLMYAFGFCSGTGLPLGYICSPAILLSALTGTFTFISLSLSALLAEQ 140
 QY 144 REYLGLGLSSGVSLFLWLFHFASSIFGSGMAVFKFELYFGLLVFVGIVYVDFDQEIIEKA 203
 Db 141 KGYLVGLGMLVSVINTMALLSLFNMFV-KSYFQVTVQLYGVGVYMAAFIVYDFQNIIVEKC 199
 QY 204 HLCMDYVXHALTFDFGAVFVRILIMLNKASEKEKKRR 247
 Db 200 RGNRVVQHALDFDVLMSFRLLIIL-----TQKEERKQNER 239

RESULT 13

ABB57985
 ID ABB57985 standard; Protein: 305 AA.

XX AC ABB57985;
 XX DT 26-MAR-2002 (first entry)
 XX XX Drosophila melanogaster polypeptide SEQ ID NO 747.
 XX DE Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX KW Drosophila melanogaster.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR N-PSDB; ABL02086.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX XX

PS Disclosure; SEQ ID NO 747; 2lpp + Sequence Listing; English.
 XX XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA
 CC sequences (ABB57737-ABB72072).
 CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX XX

SQ Sequence 305 AA;

Query Match 15.1%; Score 192; DB 22; Length 305;
 Best Local Similarity 25.7%; Pred. No. 6e-14;
 Matches 61; Conservative 49; Mismatches 87; Indels 40; Gaps 8;

QY 36 HLKQVYLTCCALVASAAGAY-----LHILNIGGLITTTMACM-----GSMVWLLSAPP 84
 Db 85 HATYAFGASCGVTAASAVAFQSDAMALMTRSGWVASLVTLGLVMSGSSIAQGLEXP 144
 QY 85 YQEQKRVALLMAALFEFASIGPLIEIGLNFDPSTVFGAFVGCACVFGCFSAAMLARR 144
 Db 145 GFGAKOLAWLVHCAVL-GAVLAPMCLLG-----GPILT KALLYTSIGIVGALSTVACAPSE 199
 QY 145 EYLYLGLGLSSGVSLFLWLFHFASSIFGSGMAVFKFELYFGLLVFVGIVYVDFDQ 197
 Db 200 KFLHMGGLAIGLVGVFASLASMWLPPTAVGAG---LASMGLYGLLFGSLFYDQ 256
 QY 198 ETEKAHLGDM-----DYVKHALTLTFDGFVVRILIMLNKASEKEKKRRN 248
 Db 257 RIVKSAELYPOYSKFYPDPINHALIYMDALNIFIRIATILAGD-----QKRKN 305

RESULT 14

ABB58798
 ID ABB58798 standard; Protein: 341 AA.

XX AC ABB58798;
 XX DT 26-MAR-2002 (first entry)
 XX XX Drosophila melanogaster polypeptide SEQ ID NO 3186.
 XX DE Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX KW Drosophila melanogaster.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR N-PSDB; ABL02901.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX XX

PS Disclosure; SEQ ID NO 3186; 2lpp + Sequence Listing; English.
 XX XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX XX

SQ Sequence 341 AA;

Query Match 13.5%; Score 172; DB 22; Length 341;
 Best Local Similarity 26.5%; Pred. No. 1.7e-11;
 Matches 56; Conservative 46; Mismatches 77; Indels 32; Gaps 9;

QY 46 CALVASAAGAYL-HILWNI---GGLITTTMACM-----GSMVWLLSAPPYQEQKRVALL 94


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Db 132 CVLTAAATFRSHRLELASGGIATIASALVTGSAVARSIEYQGLGAKHLAWA 191
QY 95 MAALFEGASIGPLIEIGINFDPISIVFAGVGCFAVFGCSAAAMLARREYLYLGGLLSSG 156
Db 192 VHCAIL-GAVIAPICFEG---GPIITRAALYTGIV-GGLSTIAACAPSKDFLYMGGLA 246
QY 155 SGVSLLF-----WLHFASISFGGSMVAFKELYFGLLVFVGYIVFDTQETIEKAHL-- 205
Db 247 IGLGVFVFASSIASMWLPPTTALGAG---LASMSLYGGLVLFSGFLLYDTQRMVRAEVP 303
QY 206 ---GMDYVVKHALITLFTDFGAVFVRILIM 232
Db 304 QYSYTPDPINASMSIYMDVINIFIRIVTIL 334

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RESULT 15

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AAB49311
ID AAB49311 standard; Protein; 346 AA.
XX
AC AAB49311;
XX
DT 01-MAR-2001 (first entry)
XX
DE Mouse brown adipose tissue clone 42 protein.
XX
KW Growth hormone; brown adipose tissue.
XX
OS Mus sp.
XX
PN W0200066784-A2.
XX
PD 09-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-0512145.
XX
PR 05-MAY-1999; 99US-0132670.
XX
PA (UYOH-) UNIV OHIO.
XX
PI Kopchick JJ, Li Y;
XX
PS WPI; 2000-665338/64.
XX

```

Diagnosis of abnormal levels of growth hormone in brown adipose tissue is carried out by monitoring the transcriptional activity of one or more genes related to growth hormone activity -

Disclosure; Page 66; 89pp; English.

The present invention provides a method of diagnosing abnormal levels of growth hormone (GH) in brown adipose tissue, by assaying the levels of specific gene transcripts. The genes of interest are those encoding glucosylphosphate isomerase, neuroleukin, pyruvate kinase, haem oxygenase, ubiquitin/ribosomal fusion protein, alpha-enolase, proteasome theta chain, trans-Golgi network protein, medium chain acyl-CoA dehydrogenase, adipocyte lipid binding protein, mitochondrial cytochrome C oxidase, mitochondrial NADH-ubiquinone oxidoreductase, mitochondrial cytochrome B or any of the genes Ng-G119K2, Ng-119K15, Ng-119K36, Ng-119K62, Ng-119K42, Ng-119K58, Ng-119K65 or Ng-119K66. This is useful for diagnosing abnormal levels of GH or predicting changes in brown adipose tissue.

Sequence 346 AA;

Query Match 13.4%; Score 171; DB 21; Length 346;

Best Local Similarity 25.9%; Pred. No. 2.2e-11;

Matches 57; Conservative 47; Mismatches 84; Indels 32; Gaps 9;

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QY 42 LTLCALVASAGAYLHIL-----W-NIGGLITTMACGSMVWLLSAPPYQEQKRVALLMA 96
Db 138 LTALSALAVARTPALMNFMTGWSVTIGATFAAMIGAGMLVHSISYEQSGPGKHLAWMLH 197

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QY 97 AALFEGASIGPLIEIGINFDPISIVFAGVGCFAVFGCSAAAMLARREYLYLGGLLSSG 156
Db 198 SGVM-GAVVAPLITIG--GPIITRAALYTGIV-GGLSTVAMCAPSEKFLNMGAPLGVG 252
QY 157 VSLLFWLHFASISFGGSM-----AVFKPELYFGLLVFVGYIVFDTQETIEKAHLG 206
Db 253 LGLV----FASSL--GSMFLPPTSVAGATLYSVAMYGGLVLFSGFLLYDTQKVIKRAEIT 306
QY 207 DM-----DYVKHALITLFTDFGAVFVRILIMLKNASEKE 240
Db 307 PMYGAQKYDPINSMIYMDVINIFIRIVTILATGSRNKK 346

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Search completed: September 22, 2003, 15:23:10
Job time : 71 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	688.5	54.1	213	4	US-09-325-932A-87	Sequence 87, Appl
2	499.5	39.3	140	4	US-09-325-932A-88	Sequence 88, Appl
3	477.5	37.5	237	2	US-08-818-514-3	Sequence 3, Appl
4	477.5	37.5	237	3	US-09-115-934A-3	Sequence 3, Appl
5	477.5	37.5	237	4	US-09-611-175-3	Sequence 3, Appl
6	165	13.0	345	4	US-09-363-133A-2	Sequence 2, Appl
7	165	13.0	345	4	US-09-995-243-2	Sequence 2, Appl
8	165	13.0	346	4	US-09-149-476-493	Sequence 2, Appl
9	120	9.4	290	4	US-09-252-991A-31434	Sequence 493, Appl
10	112.5	8.8	238	4	US-09-247-155-89	Sequence 31434, A
11	109	8.6	311	2	US-08-794-216-1	Sequence 89, Appl
12	107	8.4	369	2	US-08-749-289-1	Sequence 1, Appl
13	104	8.2	203	4	US-09-328-714A-6	Sequence 1, Appl
14	101.5	8.0	241	4	US-09-198-452A-1044	Sequence 6, Appl
15	100.5	7.9	327	4	US-09-252-991A-27652	Sequence 1044, Ap
16	96.5	7.6	257	4	US-09-372-432A-28	Sequence 27652, A
17	95.5	7.5	249	4	US-09-373-432A-30	Sequence 28, Appl
18	95	7.5	255	4	US-09-328-352-7902	Sequence 30, Appl
19	95	7.5	305	4	US-09-328-352-6794	Sequence 7902, Ap
20	94.5	7.4	516	2	US-08-794-216-3	Sequence 6794, Ap
21	94.5	7.4	516	2	US-08-749-289-3	Sequence 3, Appl
22	94	7.4	272	4	US-09-372-432A-26	Sequence 3, Appl
23	87	6.8	607	1	US-07-879-617A-12	Sequence 26, Appl
24	87	6.8	607	1	US-08-753-985-12	Sequence 12, Appl
25	85.5	6.7	426	4	US-09-252-991A-25192	Sequence 12, Appl
26	84	6.6	292	4	US-09-549-848B-32	Sequence 25192, A
27	84	6.6	316	4	US-09-328-714A-2	Sequence 32, Appl
28						Sequence 2, Appl


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; Sequence 2, Application US/09362123A
; Patent No. 6451558
; GENERAL INFORMATION:
; APPLICANT: Cooke, Michael Paul
; APPLICANT: Holness, Claire
; APPLICANT: Sirenko, Oksana
; TITLE OF INVENTION: No. 6451558el Genes in the Control of Hematopoiesis
; FILE REFERENCE: 4-30629A/SYS
; CURRENT APPLICATION NUMBER: US/09/362,123A
; CURRENT FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 09/128,310
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-362-123A-2

Query Match 13.0%; Score 165; DB 4; Length 345;
Best Local Similarity 26.3%; Pred. No. 5.3e-11;
Matches 61; Conservative 47; Mismatches 86; Indels 38; Gaps 11;

QY 36 HLKQVYLTCCALVASAAGAYLH--ILWNI---GGILT---TWACMGSMYWLISAPPYQE 87
DB 125 HSTMYVLASIGITALSATAISRTFVLMNFMGSGSWTICVTAAVMGAGNLFVRSIPYDQ 184
QY 88 Q-----KRVALLMAALPEFASIGPLIELGINFDPISIVFGAFVGCAVVGFCFSAAAMLARR 144
DB 185 SPQKHLHALLHSGVM-GAVVAPLTILG---GPLLIRAAWYTAGIV-GGLSTVAMCAPSE 239
QY 145 EYVLGLGLSSGYSLFLWLHFASISFGSM-----AVKFEELYFGILLYFVGVIYF 194
DB 240 KFLNMGAPLGVGLV---FVSSL--GSFLLPTTVAGATLISVAMIGGLVLFMSFLLY 293
QY 195 DTQIEILKAHLGDM-----DYYKHAITLFTDFGAVFVRILILMLKNASKE 240
DB 294 DTQVKIKRAEVSPMYGVQKYDPINSLSYMDTLINIFMRVATMLATGGRKK 345

RESULT 7
US-09-996-243-2
; Sequence 2, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavier, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C13

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;	CURRENT APPLICATION NUMBER:	US/09/9936,243
;	PRIOR FILING DATE:	2001-11-14
;	PRIOR APPLICATION NUMBER:	60/043787
;	PRIOR FILING DATE:	1997-06-16
;	PRIOR APPLICATION NUMBER:	60/062250
;	PRIOR FILING DATE:	1997-10-17
;	PRIOR APPLICATION NUMBER:	60/065186
;	PRIOR FILING DATE:	1997-11-12
;	PRIOR APPLICATION NUMBER:	60/065311
;	PRIOR FILING DATE:	1997-11-13
;	PRIOR APPLICATION NUMBER:	60/066770
;	PRIOR FILING DATE:	1997-11-24
;	PRIOR APPLICATION NUMBER:	60/075945
;	PRIOR FILING DATE:	1998-02-25
;	PRIOR APPLICATION NUMBER:	60/078910
;	PRIOR FILING DATE:	1998-03-20
;	PRIOR APPLICATION NUMBER:	60/083322
;	PRIOR FILING DATE:	1998-04-28
;	PRIOR APPLICATION NUMBER:	60/084600
;	PRIOR FILING DATE:	1998-05-07
;	PRIOR APPLICATION NUMBER:	60/087106
;	PRIOR FILING DATE:	1998-05-28
;	PRIOR APPLICATION NUMBER:	60/087607
;	PRIOR FILING DATE:	1998-06-02
;	PRIOR APPLICATION NUMBER:	60/087609
;	PRIOR FILING DATE:	1998-06-02
;	PRIOR APPLICATION NUMBER:	60/087759
;	PRIOR FILING DATE:	1998-06-02
;	PRIOR APPLICATION NUMBER:	60/087827
;	PRIOR FILING DATE:	1998-06-03
;	PRIOR APPLICATION NUMBER:	60/088021
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088025
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088026
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088028
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088029
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088030
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088033
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088326
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088167
;	PRIOR FILING DATE:	1998-06-05
;	PRIOR APPLICATION NUMBER:	60/088202
;	PRIOR FILING DATE:	1998-06-05
;	PRIOR APPLICATION NUMBER:	60/088212
;	PRIOR FILING DATE:	1998-06-05
;	PRIOR APPLICATION NUMBER:	60/088217
;	PRIOR FILING DATE:	1998-06-05
;	PRIOR APPLICATION NUMBER:	60/088655
;	PRIOR FILING DATE:	1998-06-09
;	PRIOR APPLICATION NUMBER:	60/088734
;	PRIOR FILING DATE:	1998-06-10
;	PRIOR APPLICATION NUMBER:	60/088738
;	PRIOR FILING DATE:	1998-06-10
;	PRIOR APPLICATION NUMBER:	60/088742
;	PRIOR FILING DATE:	1998-06-10
;	PRIOR APPLICATION NUMBER:	60/088810
;	PRIOR FILING DATE:	1998-06-10
;	PRIOR APPLICATION NUMBER:	60/088824
;	PRIOR FILING DATE:	1998-06-10
;	PRIOR APPLICATION NUMBER:	60/088826
;	PRIOR FILING DATE:	1998-06-10
;	PRIOR APPLICATION NUMBER:	60/088858
;	PRIOR FILING DATE:	1998-06-11
;	PRIOR APPLICATION NUMBER:	60/088861
;	PRIOR FILING DATE:	1998-06-11
;	PRIOR APPLICATION NUMBER:	60/088876

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RESULT 8
US/9-149-476-493
; Sequence 493, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-03-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600

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; EARLIER FILING DATE: 1997-08-22,
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 13.0%; Score 165; DB 4; Length 346;
Best Local Similarity 26.3%; Pred. No. 5.4e-11;
Matches 61; Conservative 47; Mismatches 86; Indels 38; Gaps 11;

QY 36 HLKQVYLTCCALVASAGAYLH--ILWNI--CGLLT---TWACMGSMVWLLSAPPYQE 87
DB 125 HSTYMLDAGSIGTALSAIASTFVLNFMNMGSSWVTIGVTFAMYGAGMLVRSIPYDQ 184
QY 88 Q--KRVALLMAALFEGASTGPIELGINFDPISVEGAFVGCAGVFCFSAAAMLARRR 144
DB 185 SPGPKHLAWLLHSGVM-GAVVAPLTILG--GPLLIRAAVNTAGIV-GGLSTVAMCAPSE 239
QY 145 EYLYLGLLSSGVSLFLFWLHPASSIFGSM-----AVFKFELYFGLLVFGYIVF 194
DB 240 KFLNMGAPLGVGLGV----FVSSL--GSMFLPTTVAGATLYSVAMYGGLVFSMFLLY 293
QY 195 DTQIEIKAHUGDM-----DYVKHALTLFTDFGAVFVRIILMLKNASEKE 240
DB 294 DTQKVIKRAEVSPMGYQKDYDPINSLMSIYMDTLNIFMKVATMLATGNGRKK 345

RESULT 9
US-09-252-991A-31434
; Sequence 31434, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31434
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31434

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US-08-749-289-1
 ; Sequence 1, Application US/08749289
 ; Patent No. 5955301
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Coleman, Roger
 ; TITLE OF INVENTION: NOVEL HUMAN GLUTAMATE-BINDING
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/749,289
 ; FILING DATE: Filed herewith
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PP-0160 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 855-0555
 ; TELEFAX: (415) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 369 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: Consensus
 ; CLONE: 386116
 ; US-08-749-289-1

Query Match 8.4%; Score 107; DB 2; Length 369;
 Best Local Similarity 20.8%; Pred. No. 0.00039;
 Matches 57; Conservative 41; Mismatches 90; Indels 86; Gaps 11;
 QY 2 EGFSTFFDSQSASRNRSYDSLKFNFRQISPLVQTHLKQVYLTCCALVSAAGAYLHILW 61
 DB 134 EGPPSYDNQDFPATNWDKSR-----QAFIRKVFVLTLQLSVTLSTVSVFTEV 184
 QY 50 ASAG-----AY-----LHIL-----WNIGGLTTMACGSMVWLLS 81
 DB 185 AEVKGFEVENVWTVYVSVAFFSLIVLSCCGDFRKHFNVALSVLTASLSVWGMI- 243
 QY 82 APYQEQKRVALLMAALFEGASIGPLI-ELGINFDPISVFGAFVGCVAVFCFSAAML 140
 DB 244 ASFYNTE---AVIMAVGITTAVCFWTWFSMTRYDFTSCMGVLLVSMVVFIFAILCIF 300
 QY 141 ARREYLYLGGLLSSGVSLFWLHFASSIFGSMVAFKFEYFGLLVFGYIVFTQETI 200
 DB 301 IRRN-----ILBIVAS-----LGALLFCFLAVDTQLL 330
 QY 201 --EKAHLGDMYVKHALTLFTDFGAVFVRILIIM 232
 DB 331 GNKQLSLSPFEEYVFAALNLYTDLIINFLYLII 364

RESULT 13
 US-09-328-714A-6

; Sequence 6, Application US/09328714A
 ; Patent No. 6500940
 ; GENERAL INFORMATION:
 ; APPLICANT: The Salk Institute for Biological Sciences
 ; APPLICANT: Inder M. Verma
 ; APPLICANT: Mark Schmitt
 ; APPLICANT: Nikunj V. Somia
 ; TITLE OF INVENTION: LIFE GUARD (LFG) POLYNUCLEOTIDES AND
 ; TITLE OF INVENTION: POLYPEPTIDES AND METHODS OF USE THEREOF
 ; FILE REFERENCE: SALKINS.016A
 ; CURRENT APPLICATION NUMBER: US/09/328,714A
 ; CURRENT FILING DATE: 1999-06-09
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 203
 ; TYPE: PRT
 ; ORGANISM: Drosophila
 ; US-09-328-714A-6

Query Match 8.2%; Score 104; DB 4; Length 203;
 Best Local Similarity 21.7%; Pred. No. 0.00038;
 Matches 51; Conservative 37; Mismatches 89; Indels 58; Gaps 10;
 QY 2 EGFSTFFDSQSASRNRSYDSLKFNFRQISPLVQTHLKQVYLTCCALVSAAGAYLHILW 61
 DB 18 EGTXTF-----ARNMWLF-----WVAGVWLVTLSMA-----CCSVRRQTPTNFIEL- 62
 QY 62 NIGGLTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIG-PLIELGINFDPISV 120
 DB 63 ---GLFTAAQ---SFLMGVSATKYAPKE---VLMVAVGITAACVCLATIFALQTKYDFTMM 113
 QY 121 EGAFVGCVAVFCFSAAMLARRREYLYLGGLLSSGVSLFWLHFASSIFGSMVAFKFE 180
 DB 114 GGILTIACMVVFLIFGIIVAFYVKGK-----IITLVAS----- 145
 QY 181 LVFGLLVFGVIVFTQETIIEKAH---LGDMDYVKHALTLFTDFGAVFVRILIIM 232
 DB 146 --IGALLFSVLIYDTQLMGSGEHKYSISPEYIFAALNLYTDLIINFLYLII 198

RESULT 14
 US-09-198-452A-1044
 ; Sequence 1044, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffiths, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 1044
 ; LENGTH: 241
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 ; US-09-198-452A-1044

Query Match 8.0%; Score 101.5; DB 4; Length 241;
 Best Local Similarity 23.7%; Pred. No. 0.00096;
 Matches 52; Conservative 41; Mismatches 93; Indels 33; Gaps 11;
 QY 20 YDSLKNFRQISPLVQTHLKQVY-----LTLCCALVSAAGAY--LHILNIGGLTT 69
 DB 7 YD--RDYIQDSRVQGTFSRVYGMWMTAGLIVTSCVALGLYFSGLYRSLFSEW----WVWC 60
 QY 70 MACGSMVWLLSAPPYQEQKRV-ALLMAALFEGASIGPLIEL-GINFDPISVIFGAF--- 124
 DB 61 FATLGVSFINSKIOTLSVSAVGGFLLYSTLEGMFFGLLPVYAAQYGGGVWIAFGSA 120
 QY 125 ---VGCVVVFCFSAAM--LARRREYLYLGGLLSSGVSLFWLHFASSIFGSMVAFKFE 179

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Db      121 ALVFGUAAVIGFTSOLTKISKIMTFALIGLL---VTLVF---AVVSMFVSMPLIYL 174
QY      180 ELYFGLLVFVGIVFTQETIIE-KAHLGDMQVVKHALTL 217
Db      175 ICYGLVIVFVGLTAADAQAIRRISSITIGDNNILSYKLSL 213

RESULT 15
US-09-252-991A-27652
; Sequence 27652, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27652
; LENGTH: 327
; TYPE: PRY
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27652

Query Match      7.9%; Score 100.5; DB 4; Length 327;
Best Local Similarity 23.7%; Pred. No. 0.0019;
Matches 54; Conservative 28; Mismatches 65; Indels 81; Gaps 11;

QY      31 PLVQTHLKQVYTLCCALVASAAGAYLHLMWIGGLLT-----MACMGSM 76
Db      4  PLAQA-----HLRACRAALALTAMPLOSLNLSRILLRGISQVFLQDPRLGLACL--L 57
QY      77 VWLLSAPPYQOKRVALLMAALFEGASTGPL-----IELGINFDSIVFGAFV 125
Db      58 AIYVGAPP-----LLAGALLGA-LGPLLRLHLCADSIEAGLYGYNAVLIGMLL 107
QY      126 G-----CAVVGCFSAAML-----ARREYL--YLGGLSSG---VSLLPWLH 164
Db      108 AFRFAWSPGLVSLVALGCLASVALQRLFLHGLRRRRWLPPTTLGFLVNGWLVPLGAMLG 167
QY      165 FASSIFGGSMA-----VFKEFYGLLVFVGIV 193
Db      168 LAPATHGGCFSCAWSGTAEALAAQIGETIFLGEPLAGLLVWLGLLL 215
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Search completed: September 22, 2003, 15:19:35
Job time : 45 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:20:33 ; Search time 27 Seconds
(without alignments)
1367.613 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGFTSFDSQASNRWSY.....LIIMLNASEKEKKKKRRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: .556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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6: /cgn2_6/ptodata/2/pubpaa/FCIUS_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1272	100.0	248	11	US-09-955-526-4
2	988	77.7	244	15	US-10-167-015-16
3	963.5	75.7	247	15	US-10-219-220-274
4	935	75.1	261	15	US-10-167-015-18
5	884.5	69.5	252	15	US-10-167-015-32
6	878.5	69.1	258	15	US-10-167-015-34
7	878.5	69.1	255	15	US-10-167-015-6
8	853	67.1	252	15	US-10-167-015-4
9	786.5	61.8	250	15	US-10-167-015-2
10	772.5	60.7	255	15	US-10-219-220-273
11	688.5	54.1	213	15	US-10-219-220-87
12	499.5	39.3	140	15	US-10-219-220-88
13	491.5	38.6	236	12	US-10-263-828-74
14	484.5	38.1	141	15	US-10-167-015-8
15	483.5	38.0	255	9	US-09-925-302-516

16	339	26.7	78	15	US-10-167-015-20	Sequence 20, Appli
17	301	23.7	162	12	US-10-002-631C-4	Sequence 4, Appli
18	185	13.0	345	9	US-09-745-763-68	Sequence 68, Appli
19	185	13.0	345	9	US-09-989-722-2	Sequence 2, Appli
20	185	13.0	345	9	US-09-989-723-2	Sequence 2, Appli
21	185	13.0	345	9	US-09-989-279-2	Sequence 2, Appli
22	185	13.0	345	9	US-09-989-727-2	Sequence 2, Appli
23	185	13.0	345	10	US-09-989-731-2	Sequence 2, Appli
24	185	13.0	345	10	US-09-989-732-2	Sequence 2, Appli
25	185	13.0	345	10	US-09-991-073-2	Sequence 2, Appli
26	185	13.0	345	10	US-09-990-442-2	Sequence 2, Appli
27	185	13.0	345	10	US-09-991-163-2	Sequence 2, Appli
28	185	13.0	345	10	US-09-993-604-2	Sequence 2, Appli
29	185	13.0	345	10	US-09-990-456-2	Sequence 2, Appli
30	185	13.0	345	10	US-09-989-721-2	Sequence 2, Appli
31	185	13.0	345	10	US-09-992-598-2	Sequence 2, Appli
32	185	13.0	345	10	US-09-989-293A-2	Sequence 2, Appli
33	185	13.0	345	10	US-09-989-735-2	Sequence 2, Appli
34	185	13.0	345	10	US-09-990-444-2	Sequence 2, Appli
35	185	13.0	345	10	US-09-991-181-2	Sequence 2, Appli
36	185	13.0	345	10	US-09-989-730-2	Sequence 2, Appli
37	185	13.0	345	10	US-09-990-436-2	Sequence 2, Appli
38	185	13.0	345	10	US-09-993-687-2	Sequence 2, Appli
39	185	13.0	345	11	US-09-989-734-2	Sequence 2, Appli
40	185	13.0	345	11	US-09-997-653-2	Sequence 2, Appli
41	185	13.0	345	11	US-09-993-667-2	Sequence 2, Appli
42	185	13.0	345	11	US-09-997-428-2	Sequence 2, Appli
43	185	13.0	345	11	US-09-997-666-2	Sequence 2, Appli
44	185	13.0	345	11	US-09-990-438-2	Sequence 2, Appli
45	185	13.0	345	11	US-09-990-562-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-955-526-4
; Sequence 4, Application US/09955526
; Publication No. US20030009785A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Plant Cytoprotective Genes and Methods
; FILE OF INVENTION: of Using Same
; FILE REFERENCE: P-LJ 4868
; CURRENT APPLICATION NUMBER: US/09/955,526
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/661,014
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-955-526-4

Query Match 100.0%; Score 1272; DB 11; Length 248;
Best Local Similarity 100.0%; Pred. No. 7.2e-129;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGFTSFDSQASNRWSYDSLKNPQISPLVQTHLKQVYLTLCALVASAAGAYLHL 60
Db 1 MEGFTSFDSQASNRWSYDSLKNPQISPLVQTHLKQVYLTLCALVASAAGAYLHL 60
QY 61 WNIIGGLTTMACGSMVWLLSAPPYQOKRVALLMAALFEGASIGPLIEIGTNPDPSTV 120
Db 61 WNIIGGLTTMACGSMVWLLSAPPYQOKRVALLMAALFEGASIGPLIEIGTNPDPSTV 120
QY 121 FGAFVGCAYVFCFSAAMLRREYLYLGGLLSSGVSLFLFWLHFASSIFGSGMAVFKFE 180
Db 121 FGAFVGCAYVFCFSAAMLRREYLYLGGLLSSGVSLFLFWLHFASSIFGSGMAVFKFE 180
QY 181 LYPGLLVFVGYYIVDFQETIEIKAHGLGMDYVVKHALFTDFGAVFVRILLIMLNASEKE 240

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Db 181 LYFGLLVFGVIVDTQEIIEKAHLGDMYVKKHALTFTDFGAVFVRILIIIMLKNAEKE 240
QY 241 EKKKKRRN 248
Db 241 EKKKKRRN 248

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RESULT 2

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US-10-167-015-16
; Sequence 16, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Glycine max
US-10-167-015-16

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Query Match 77.7%; Score 988; DB 15; Length 244;
Best Local Similarity 75.5%; Pred. No. 2.8e-98;
Matches 185; Conservative 32; Mismatches 24; Indels 4; Gaps 1;

QY 4 FTSFDSQASRNRWSYDLSKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHLWNI 63
Db 4 FNSFED---SRNRWYDTLKNFRQISPVQNHKLQVYTLTCAVVAAGAYLHLWNI 59

QY 64 GLLTTMACGSMWLLSAPPYQEQKRVALLMAALFEGASIGPLIEGINFDPSPVFGA 123
Db 60 GGLTTVACGSSFWLLSTPPEERKRVTLMAASLFGSGSIGPLIDIAIHDPSPVFGA 119

QY 124 FVGCVAVFGCSAAAMLARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKFELYF 183
Db 120 FVGTALAFACFSGAALVARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKFELYF 179

QY 184 GLLVFGVIVDTQEIIEKAHLGDMYVKKHALTFTDFGAVFVRILIIIMLKNAEKEKK 243
Db 180 GLLVFGVIVDTQEIIEKAHLGDMYVKKHALTFTDFGAVFVRILIIIMLKNAEKEKK 239

QY 244 KKKRN 248
Db 240 KKKRD 244

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RESULT 3

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US-10-219-220-274
; Sequence 274, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 274
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-274

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Query Match 75.7%; Score 963.5; DB 15; Length 247;
Best Local Similarity 74.4%; Pred. No. 1.3e-95;
Matches 186; Conservative 27; Mismatches 32; Indels 5; Gaps 2;

QY 1 MEGTSPFDSQASRNRWSYDLSKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 60
Db 1 MDAFASLFQS---SGKGWSDSLKNFRQISPAVOSHLKANVYLSLCCALMASAGAYLHL 57

QY 61 WNIIGLLTTMACGSMWLLSAPPYQEQKRVALLMAALFEGASIGPLIEGINFDPSPV 120
Db 58 LNIIGLLTTIACIGSIWVLLSIPPHEOKRGLLMAALFEGACIGPLIDIAIKVDPSPV 117

QY 121 FGAIVGCAVFGCSAAAMLARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKFE 180
Db 118 ISAFVGSALAFACFSGAALVARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKFE 177

QY 181 LYFGLLVFGVIVDTQEIIEKAHLGDMYVKKHALTFTDFGAVFVRILIIIMLKNAEKE 240
Db 178 IYFGLLVFGVIVDTQEIIEKAHLGDMYVKKHALTFTDFGAVFVRILIIIMLKNAEKE 237

QY 241 --EKKKKRRN 248
Db 238 KNEKKKKRED 247

```

RESULT 4

```

US-10-167-015-18
; Sequence 18, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Glycine max
US-10-167-015-18

```

```

Query Match 75.1%; Score 955; DB 15; Length 261;
Best Local Similarity 73.3%; Pred. No. 1.1e-94;
Matches 178; Conservative 36; Mismatches 27; Indels 2; Gaps 1;

QY 6 SFEDSQ--SASRNRWSYDLSKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHLWNI 63
Db 3 TFFNSQSSSSRSRWSYDLSKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHLWNI 62

QY 64 GLLTTMACGSMWLLSAPPYQEQKRVALLMAALFEGASIGPLIEGINFDPSPVFGA 123
Db 63 GGLTTIACIGSIWVLLSTPPEERKRVTLMAASLFGSGSIGPLIDIAIAIDPSLIVA 122

QY 124 FVGCVAVFGCSAAAMLARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKFELYF 183
Db 123 FVATSLAFACFSGAALVARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKFELYF 182

```

184	QY	GLLVFVGIVFDQTQEIIEKAHLGDMDVVKHALTLFTD	FGAVFVRILIIIMLNASEKEPKK	243
183	Db	GLLVFVGIVFDQTQEIIEAHLFGDGVVKHALTLFTD	LAALFVRILIIIMLNSEGGNGKK	242
244	QY	KKR	246	
243	Db	KKR	245	

```

RESULT 5
US-10-167-015-32
; Sequence 32, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-32

```

[illegible]

```

RESULT 6
US-10-167-015-34
; Sequence 34, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015

```

```

; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 258
; TYPE: prt
; ORGANISM: zea mays
; US-10-167-015-34

```

```

Query Match          69.1%; Score 878.5; DB 15; Length 258;
Best Local Similarity 65.8%; Pred. No. 1.9e-86;
Matches 169; Conservative 37; Mismatches 42; Indels 9; Gaps 3;

QY 1 MEGFTSFDDSQSASR-----NRWSDYSLKNFRQISPLVQTHLKQVYLTLCALVASAA 53
Db 1 MDAFYSTTASSTSSAPYGGGGCGWGYDSMKNFQISPAVQTHLKLVLTLCVALASSAV 60

QY 54 GAYLHLNWNIGGLLTTMACGSMVWVLSAPPYQOKRVALIMAAALFEGASIGPLIELGI 113
Db 61 GAYLHVWNIGGMLTMLGCGVGSIAWLFSPVYEERKRYWLLMAAALLFEGASVGPLIKLV 120

QY 114 NFDPISVFGAFGCVAVFGFCFSAAAMLARREYLYLGLGLSSGVSLFLWLHFASSIFG-G 172
Db 121 EFDPSILVTAFVGTAFIAFACFSCAAMVAKRREYLYLGLGLSSGISLLWLQFPAASIFGHQ 180

QY 173 SMAVFKEFLYGLLVFVGYIVFDQETIEKHLGDMQYVVKHALTLFTDFDGFVAVRILIM 232
Db 181 STSFSFEVYFGLLIIFLGYMYIDQEVIERAHGDMYIKHALTLFTDFDFAVLVRLIVIM 240

QY 233 LKNASEK-EKKKKRRN 248
Db 241 LKNAADKSDKKRRRS 257

```

```

RESULT 7
US-10-167-015-6
; Sequence 6, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 285
; TYPE: PRT
; ORGANISM: zea mays
US-10-167-015-6

```

```
Query Match      69.1%; Score 878.5; DB 15; Length 205;
Best Local Similarity 65.8%; Pred. No. 2.2e-86;
Matches 169; Conservative 37; Mismatches 42; Indels 9; Gaps 3;
```



```

QY 115 FDPSTVGFAGVCAVVGCFSAAMLARREYLYLGGLLSGVSLFWLHFASSTFGSGM 174
; SEQ ID NO 88
; LENGTH: 140
; TYPE: PRT
Db 121 IDSSILNSAFVGTSAFACFAAATARRREYLFGLGSGSISLMLWLASSIFGSGS 180
; ORGANISM: Pinus radiata
; US-10-219-220-88
QY 175 AVFKFELFGLLVFGYIVFTDQETIEKAHLGDMDYVVKHALTLFTDFGAVFVRILIMLK 234
; Query Match 39.3%; Score 499.5; DB 15; Length 140;
; Best Local Similarity 66.2%; Pred. No. 6e-46;
; Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;
Db 181 AIYTEIFVGLLVFGYIIFDTQMIIEKADHGXDYLKSLDLFDFFVAVFVRLVIMAK 240
; MEGFTSFEDSASRNRSYDSLKNFRQISPLVQVTHLKQVYLTCCALVSAAGAYLHL 60
; 1 MDAFASLFQS---SGKWSHSDSLKNFRQISPAVQSHLKNVYLSLCCALMASAGAYLHL 57
QY 235 NA-SEKEKKKKRR 247
; Db 241 NADSKSREGKKRR 254
; 61 WNIIGLLTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIEGINFDPSTV 120
; 58 LNIIGLLTTIACIGSIVWLLSIPPEBQKRFGLLMAALFEGACIGPLIEAIAIKVDPSIV 117
; 121 FGAVGCNAVFGCFSAAMLARREYLYLGG 151
; 118 ISAFVGSALAFACFSGA-----CWLGG 140
; US-10-219-220-87
; Sequence 87, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Pinus radiata
; US-10-219-220-87
Query Match 54.1%; Score 688.5; DB 15; Length 213;
Best Local Similarity 64.6%; Pred. No. 4.5e-66;
Matches 137; Conservative 31; Mismatches 41; Indels 3; Gaps 2;
QY 39 QVYLTLCCALVSAAGAYLHLIWNIGLLTTMACGSMVWLLSAP--PYQKQKRVALLMA 96
; 1 RYVLSLCAVTAATGVYVYLLHLLNIGLLTGLACIGSVIGLISVPTSNNECKRAALLLA 60
; 97 AALFEGASIGPLIEGINFDPSTVGFAGVCAVVGCFSAAMLARREYLYLGGLLSG 156
; 61 AAAPKGAITPLIDAVINIDSSILVSFAVGTSLAFACFAAATARRREYLFGLGSG 120
; 157 VSLFLFWLHFASIFGSGMAVFKFELYLGLLVFGYIVFTDQETIEKAHLGDMDYVVKHALT 216
; 121 ISILMLQLASSIFGSGSAITFEYIFGLLVFGYIIFDTQMIIEKADHGXDYLKSLD 180
; 217 LFTDGAVFVRILIMLKNA-SEKEKKKKRR 247
; 181 LFDFAVAVFVRLVIMAKNADSKSREGKKRR 212
; US-10-219-220-88
; Sequence 88, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0

```

```

; SEQ ID NO 88
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Pinus radiata
; US-10-219-220-88
Query Match 39.3%; Score 499.5; DB 15; Length 140;
Best Local Similarity 66.2%; Pred. No. 6e-46;
Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;
QY 1 MEGFTSFEDSASRNRSYDSLKNFRQISPLVQVTHLKQVYLTCCALVSAAGAYLHL 60
; 1 MDAFASLFQS---SGKWSHSDSLKNFRQISPAVQSHLKNVYLSLCCALMASAGAYLHL 57
; 61 WNIIGLLTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIEGINFDPSTV 120
; 58 LNIIGLLTTIACIGSIVWLLSIPPEBQKRFGLLMAALFEGACIGPLIEAIAIKVDPSIV 117
; 121 FGAVGCNAVFGCFSAAMLARREYLYLGG 151
; 118 ISAFVGSALAFACFSGA-----CWLGG 140
; US-10-263-828-74
; Sequence 74, Application US/10263828
; Publication No. US20030138905A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: mammary gland and methods for their use.
; FILE REFERENCE: 11000.1044U1con
; CURRENT APPLICATION NUMBER: US/10/263,828
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Bovine
; US-10-263-828-74
Query Match 38.6%; Score 491.5; DB 12; Length 236;
Best Local Similarity 42.9%; Pred. No. 8.7e-45;
Matches 99; Conservative 53; Mismatches 72; Indels 7; Gaps 4;
QY 19 SYDSLKNFRQISPLVQVTHLKQVYLTCCALVSAAGAYLHLIWNL--GGLLTTMACGSM 76
; 9 NFDALFKESHITPSTQOHLKKVYASFALCMFVAAGAYLHVYTHFIQAGLLSALGSLGM 68
; 77 VWLSAPPYQ--EQKRVALLMAALFEGASIGPLIEGINFDPSTVGFAGVCAVVGCF 134
; 69 IWLMTAPSHETEQRKRLGGLAGFAFLTGVLGSPALDLCITAINPSILPTAFMGTAIETCF 128
; 135 SAAAMLARREYLYLGGLLSSGVSLFWLHFASSTFGSGMAVFKFELYLGVYIVF 194
; 129 TLSALYARRRSYLFGLGIIIMSAISLML--LSSIGNLFFGSMVLFQANLTVGLVVMCGFVLF 187
; 195 DTQEIIIEKAHLGDMDYVVKHALTLFTDFGAVFVRILIMLKNASEKEKKKK 245
; 188 DTQLIIIEKAENGDKDYIWHCVDFLDFVTLFRKLMILAMN--EKDKKKKK 236
; US-10-167-015-8
; Sequence 8, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kaun, William J.
; RESULT 14
; US-10-167-015-8
; Sequence 8, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kaun, William J.

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:17:39 ; Search time 43 seconds

(without alignments)
 554.647 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGTSPFDQSASNRNWSY.....LIIMLKNAKEKKKKRRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 145 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023.5	80.5	247	T52449	Bax inhibitor-1 (i
2	479	37.7	236	S42069	TEGT protein - rat
3	472	37.1	261	E71445	hypothetical prote
4	472	37.1	262	A85197	TEGT protein homol
5	471.5	37.1	237	I38334	TEGT (testis enhan
6	170.5	13.4	219	A10628	probable membrane
7	157.5	12.4	219	D85624	probable carrier/t
8	157.5	12.4	219	F90760	probable carrier/t
9	157.5	12.4	219	S07180	probable glutamate
10	144	11.3	266	T41414	probable receptor-
11	143.5	11.3	342	T34438	hypothetical prote
12	143	11.2	297	S63281	probable membrane
13	136.5	10.7	245	A83484	integral membrane
14	130.5	10.3	238	E81729	conserved hypothet
15	128.5	10.1	238	E71467	probable transport
16	128	10.1	236	A10142	probable membrane
17	124.5	9.8	239	T48120	hypothetical prote
18	124	9.7	231	A75462	conserved hypothet
19	123.5	9.7	231	D81441	probable integral
20	122	9.6	234	B64815	ybhl protein - Esc
21	122	9.6	234	H90736	hypothetical prote
22	122	9.6	234	A85587	hypothetical prote
23	121.5	9.6	239	Q0BEG5	HWLF2 protein - hu
24	120	9.4	222	S38835	probable glutamate
25	120	9.4	422	H64489	hypothetical prote
26	114.5	9.0	220	A64141	probable glutamate
27	114	9.0	227	G81014	conserved hypothet
28	113	8.9	223	D82210	conserved hypothet
29	112.5	8.8	230	H64634	conserved hypothet

30	112	8.8	232	2	AH0954	probable membrane
31	109.5	8.6	230	2	F71879	hypothetical prote
32	109	8.6	260	2	A12905	conserved hypothet
33	109	8.6	260	2	B97681	hypothetical prote
34	108.5	8.5	236	2	H71724	hypothetical prote
35	106	8.3	659	2	AB1293	ABC transporter (p
36	104	8.2	203	2	S53708	N-methyl-D-aspart
37	103.5	8.1	670	2	AH1664	ABC transporter (p
38	101.5	8.0	225	2	AG1350	hypothetical prote
39	101.5	8.0	236	2	E97723	hypothetical prote
40	101.5	8.0	238	2	H86611	transport permease
41	101.5	8.0	238	2	A72013	transport permease
42	99.5	7.8	225	2	AB1721	hypothetical prote
43	99.5	7.8	248	2	T01080	hypothetical prote
44	99	7.8	231	2	D97248	conserved membrane
45	98.5	7.7	511	2	JC7692	oligodendrocyte tr

ALIGNMENTS

RESULT 1

T52449

Bax inhibitor-1 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000

C:Accession: T52449

R:Kawai, M.; Pan, L.; Reed, J.C.; Uchimiya, H.

FEBS Lett. 464, 143-147, 1999

A:Title: Evolutionally conserved plant homologue of the Bax Inhibitor-1 (BI-1) gene c

A:Reference number: Z26078

A:Accession: T52449

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-247 <KAW>

A:Cross-references: EMBL:AB025927; PIDN:BAA89541.2

A:Experimental source: cultivar Columbia

C:Genetics:

A:Gene: AtBI-1

C:Function:

A:Description: suppresses cell death induced by Bax

C:Superfamily: human testicular protein TEGT

Query Match	80.5%	Score 1023.5;	DB 2;	Length 247;
Best Local Similarity	77.4%;	Pred. No. 1.4e-85;		
Matches 192;	Conservative 31;	Mismatches 24;	Indels 1;	Gaps 1;
QY	1	MEGFTSPFDQSASNRNWSYDSLKKNFRQISPLVQTHLKQVYTLCCALVASAAGAYLHL	60	
Db	1	MDAFSFFDSQPGSRS-WSYDSLKKNFRQISPAVQNLKRVYTLCCALVASAFAYLHV	59	
QY	61	NNIGILLTMTACGSMVWLLSAPPYQOKRVALLMAALFEAGSTGLIELGDFDPSTV	120	
Db	60	NNIGILLTIGTGIMWLLSCPPYEHQKRSLLFVSAVLEGSVGLIKKVAIDVPSLL	119	
QY	121	FOAFVGCVAVFCFSAAAMLARREYLYLGLLSGSVSLLEWHPASSIFGGSMAVFKFE	180	
Db	120	ITAFVGTATAFVCFSAAMLARREYLYLGLLSGSVSLLEWHPASSIFGGSMAVFKFE	179	
QY	181	LYFGLLVFGYIVFTQETIEIKAHGLGDMYVKAHLTLTDFGAVFVRILIMLKNAKE	240	
Db	180	LYFGLLVFGYIVFTQETIEIKAHGLGDMYVKAHLTLTDFGAVFVRILIMLKNAKE	239	
QY	241	EKKKKRRN	248	
Db	240	EKKKKRRN	247	

RESULT 2

S42069

TEGT protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: D85624

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-219 <STO>

A;Cross-references: GB:AE005174; NID:g12514158; PIDN:AAG55456.1; GSPDB:GN00145; UWGP:

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: yccA

C;Superfamily: Escherichia coli ybH protein

Query Match 12.4%; Score 157.5; DB 2; Length 219;

Best Local Similarity 26.7%; Pred. No. 5.9e-07;

Matches 64; Conservative 45; Mismatches 80; Indels 51; Gaps 11;

QY 12 SASNRNWSYDSLKNFROISPLVOTH--LKQVY--LTCCALVASAGAYLHLIWNIGLL 67

DB 6 SSSHDRTS-----LLSTHKVLRNTYFLLSLTAFSAITATASTVLMPLSPGLI 53

QY 68 TTNACGSMYLLSAPPYQOKRVALIIMAAAL--FEGASIGPIELGINF--PSIVGAF 124

DB 54 LTLVGMGLMFLYK---MANKPTGIISAFATCGFLGYILGPILNTVLSAGMGDVIMAL 110

QY 125 VGCVAVFGCFSAAMLARREYLYLGGLLSSGVSLLF-----WLHFASSIFGG 172

DB 111 GGTALVFFCCS-AVLTTRKDMSFGLGMLMAGIIVVVLGMVANIFLQLPALHLAIS---- 165

QY 173 SMAVFKFELFGLLVFVGYIVFTDQETIEIKAHLCGDMYVKHALTLTFDGCAGVFRILIM 232

DB 166 --AVF-----ILISSGAILFETSNII---HGGETNYIRATVSLVSLYNIEFVLSLSIL 213

RESULT 8

F90760

probable carrier/transport protein ECs1054 [imported] - Escherichia coli (strain O157:H7)

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Aug-2002

C;Accession: F90760

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and G

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: F90760

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-219 <RAY>

A;Cross-references: GB:BA000007; PIDN:BA34477.1; PID:g13360514; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs1054

C;Superfamily: Escherichia coli ybH protein

Query Match 12.4%; Score 157.5; DB 2; Length 219;

Best Local Similarity 26.7%; Pred. No. 5.9e-07;

Matches 64; Conservative 45; Mismatches 80; Indels 51; Gaps 11;

QY 12 SASNRNWSYDSLKNFROISPLVOTH--LKQVY--LTCCALVASAGAYLHLIWNIGLL 67

DB 6 SSSHDRTS-----LLSTHKVLRNTYFLLSLTAFSAITATASTVLMPLSPGLI 53

QY 68 TTNACGSMYLLSAPPYQOKRVALIIMAAAL--FEGASIGPIELGINF--PSIVGAF 124

DB 54 LTLVGMGLMFLYK---MANKPTGIISAFATCGFLGYILGPILNTVLSAGMGDVIMAL 110

QY 125 VGCVAVFGCFSAAMLARREYLYLGGLLSSGVSLLF-----WLHFASSIFGG 172

DB 111 GGTALVFFCCS-AVLTTRKDMSFGLGMLMAGIIVVVLGMVANIFLQLPALHLAIS---- 165

QY 173 SMAVFKFELFGLLVFVGYIVFTDQETIEIKAHLCGDMYVKHALTLTFDGCAGVFRILIM 232

DB 166 --AVP-----ILISGAILFETSNI--HGGETNVRATVSLVSLNIFVLSLIL 213

RESULT 9

S07180

probable glutamate receptor yccA - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002

C:Accession: S07180; A64838

R:Tamura, F.; Nishimura, S.; Ohki, M.

EMBO J. 3, 1103-1107, 1984

A:Title: The E. coli dive mutation, which differentially inhibits synthesis of certain P

A:Reference number: S07180; MUID:84236106; PMID:6376117

A:Accession: S07180

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-219 <TM>

A:Cross-references: EMBL:X00547; NID:g41283; PIDN:CAA25218.1; PID:g41284

A:Experimental source: strain W3110

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A64838

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-219 <BLAT>

A:Cross-references: GB:AE000199; GB:U00096; NID:g1787202; PIDN:AAC74056.1; PID:g1787205;

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: yccA

A:Map position: 22 min

C:Superfamily: Escherichia coli ybhL protein

C:Keywords: transmembrane protein

F:26-42/Domain: transmembrane #status predicted <TM1>

F:43-59/Domain: transmembrane #status predicted <TM2>

F:75-91/Domain: transmembrane #status predicted <TM3>

F:105-121/Domain: transmembrane #status predicted <TM4>

F:138-154/Domain: transmembrane #status predicted <TM5>

F:162-178/Domain: transmembrane #status predicted <TM6>

F:200-216/Domain: transmembrane #status predicted <TM7>

Query Match 12.4%; Score 157.5; DB 2; Length 219;

Best Local Similarity 27.0%; Pred. No. 5.9e-07;

Matches 65; Conservative 46; Mismatches 77; Indels 53; Gaps 12;

QY 12 SASRRNWSYSLKNFRQISPLVQTH--LKQVY--LTLCALVASAAGAYLHLWNIGLL 67

DB 6 SSSHDRTS-----LLSTHKVLRNTYFLLSLTALFSAITATASTVLMFLPGLI 53

QY 68 TTMACGSMVWLLSAPPYQ-RQKRVALLMAAL--FEGASIGPLIEIGINFD-PSIVFGA 123

DB 54 LTLVGMGLMFL---TYKTANKPTGIISAFATGFLGYILGPIILNTVLSAGMGDIVAMA 109

QY 124 RVGCAVVGFCFSAAMARRREYLYLGLLSSGVSLF-----WLHPASSIFG 171

DB 110 LGGTALVFCCS-AVLTTRKDMSPFLGMLMAGIVVVLGMVANFLQIPALHLAIS--- 165

QY 172 GSMAYFKFELVGLIVFVGYIVFDQETIEKAHLGDMYVVKHALTLFTDFGAVFVRILII 231

DB 166 ---AVF-----ILISGAILFETSNI--HGGETNVRATVSLVSLNIFVLSLIL 212

QY 232 M 232

DB 213 L 213

RESULT 10

T41414

probable receptor-associated protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T41414

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.

submitted to the EMBL Data Library, September 1998

A:Reference number: Z21954

A:Accession: T41414

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-266 <WOO>

A:Cross-references: EMBL:AL031798; PIDN:CAA21183.1; GSPDB:GN00068; SPDB:SPCC576.04

A:Experimental source: strain 972h; cosmid c576

C:Genetics:

A:Gene: SPDB:SPCC576.04

A:Map position: 3

Query Match 11.3%; Score 144; DB 2; Length 266;

Best Local Similarity 24.9%; Pred. No. 1.2e-05;

Matches 65; Conservative 39; Mismatches 95; Indels 62; Gaps 14;

QY 10 SOSASRRNWSYSLKNFRQISPLVQ-----THLKQVYLTLCAL-VASAAGA--YLHI 59

DB 29 NESATEN-----PAVDQFKNTTPVAECAKSIRMAFLRKVYAILTAQLFVTSFLGGIFLHP 84

QY 60 LWN-----IGLLTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPL 108

DB 85 AFSEWQMPHPLILNFFISLVILFG-----LIMKPYSPRNYIFLFLTALEGLTGA 139

QY 109 IELGINFEDPSIVFGAFVGCVAVFGCFA--AAMLARREYLYLGLLSSGV-----SLL 160

DB 140 ITF---FSARIILEAVF---ITLGVFEVALTFTQSKWDFSLGGLFVLSLILTLPI 193

QY 161 FWL-----HFASSIFGSGMAVFKFELYFGLIVFVGYIVFDQETIEKAHLGDMYVVKHALT 216

DB 194 FFEVFPSTPFIDMAFAG-----FGLTVFCGYILEDTYNILHR--YSPEEFIMSLM 241

QY 217 LFTDFGAVFVRILII--MLKN 235

DB 242 LYLDFINLFIQLQLGLMLQN 262

RESULT 11

T34438

hypothetical protein K11H12.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T34438

R:Bradshaw, H.

submitted to the EMBL Data Library, February 1997

A:Description: The sequence of C. elegans cosmid K11H12.

A:Reference number: Z21526

A:Accession: T34438

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-342 <BRA>

A:Cross-references: EMBL:U88168; PIDN:AAC24403.1; GSPDB:GN00022; CESP:K11H12.8

A:Experimental source: strain Bristol N2; clone K11H12

C:Genetics:

A:Gene: CESP:K11H12.8

A:Map position: 4

A:Introns: 45/3; 67/1; 150/3; 186/1; 262/1; 314/2

Query Match 11.3%; Score 143.5; DB 2; Length 342;

Best Local Similarity 23.7%; Pred. No. 1.7e-05;

Matches 51; Conservative 47; Mismatches 86; Indels 31; Gaps 8;

QY 42 LTLCALVASAAGAYLHLWNIGLLTTMACGSMVWL--LSAPPYQEQKRVALLMAAL- 99

DB 126 LTAVGVAASRAAIRMRLTAG--GMMSLFGTMAAMIASGMLARSIDYESTVAKHLAWALH 184

QY 100 --FEGASIGPLIEIGINFDPSIVFGAFVGCVAVFGCFSAAAMLARREYLYLGLLSSGV 157

DB 185 GGVLGAVFAPLCFMA--GPVLTRAAAWYTAGIV--GGLSATATAPSEKFLMMSGLAMGF 240

QY 158 SLLFWLHPAS-----SIFGGSMAYFKFELYFGLIVFVGYIVFDQETIEKA----- 203

```

Db 241 GVVFANIGAFPLPGSALGASLA--SIVVYGLILFSAFLYDQRLVKKAEHNPHPSQ 298
      ::::: : : : | | | | : | | | | : | | | | : | | | |
QY 204 -----HLGDMYVVKHATLFTDFGAVFVRILLIM 232
      : : : : : : : : : : : : : : : : : : : : : :
Db 299 LYGSDMQIRSFDPINQMSIYMDVLNIFMRUYMIM 333
      : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
S63281
probable membrane protein YNL305c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein N0405
C:Species: Saccharomyces cerevisiae
C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
A:Reference number: S63281; S60395; S66127
R:Maurer, C.T.C.; Urbanus, J.H.M.; Planta, R.J.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63266
A:Accession: S63281
A:Molecule type: DNA
A:Residues: 1-297 <MAU>
A:Cross-references: EMBL:271581; NID:g1302402; PID:e239757; PID:g1302403; MIPS:YNL305c
R:Maurer, K.C.T.; Urbanus, J.H.M.; Planta, R.J.
Yeast 11, 1303-1310, 1995
A:Title: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a
C, and a novel putative serine/threonine protein kinase gene.
A:Reference number: S60394; MUID:96132033; PMID:8553702
A:Accession: S60395
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-297, 'D', <MAU>
A:Cross-references: EMBL:023084
R:Maurer, K.T.C.
submitted to the EMBL Data Library, March 1995
A:Reference number: S66127
A:Accession: S66127
A:Molecule type: DNA
A:Residues: 1-297 <MAU>
A:Cross-references: EMBL:U23084; NID:g1050853; PID:g1050855
C:Genetics:
A:Map position: 14L
A:Cross-references: SGD:S0005249
C:Keywords: transmembrane protein
F:86-102/Domain: transmembrane #status predicted <TM1>
F:173-189/Domain: transmembrane #status predicted <TM2>
F:212-228/Domain: transmembrane #status predicted <TM3>
F:238-254/Domain: transmembrane #status predicted <TM4>
F:271-287/Domain: transmembrane #status predicted <TM5>

Query Match 11.2%; Score 143; DB 2; Length 297;
Best Local Similarity 24.3%; Pred. No. 1.7e-05;
Matches 65; Conservative 44; Mismatches 83; Indels 76; Gaps 13;
QY 31 PLV-OTHLKQVYLTCCALVASAAGY-----LHI-LWNIGLLITTMACMGS 75
      : : : : : : : : : : : : : : : : : : : : : :
Db 44 PLIQRHFHKYVLSLSCQLLASLSPCYWASVSTSLQNTFMSHIALFYICMVSLSVC--- 100
      : : : : : : : : : : : : : : : : : : : : : :
QY 76 MWVLLSAP-----PYEQKR-----VALLMAAALFEGA 103
      : : : : : : : : : : : : : : : : : : : : : :
Db 101 -IWLAVSRPEDYASVPEPLLTGSSEPAQEORPLPHVYLSYKQKTLISIFTLSEAY 159
      : : : : : : : : : : : : : : : : : : : : : :
QY 104 STGPIELGINDPISIVFGAVGVCFAAAMARREYLYLGLLSSGVSLFLWL 163
      : : : : : : : : : : : : : : : : : : : : : :
Db 160 CILS-LVTLA--YDKDVLISALLITIVVGVSLTALSER-----FENVLSATSIYWL 210
      : : : : : : : : : : : : : : : : : : : : : :
QY 164 HF-----ASSIFGSMVAFKELYFGLL---VFVGIVFTQELIEKAHLGDMY 210
      : : : : : : : : : : : : : : : : : : : : : :
Db 211 NWGLIMTGMGTLALGWNTSHSSKNFLYGLWGLAITAYLFDITQLIFRKYV--PDDE 268
      : : : : : : : : : : : : : : : : : : : : : :
QY 211 VKHALTFTDFGAVFVRILLIMLNASE 238
      : : : : : : : : : : : : : : : : : : : : : :
Db 269 VRCAMWLYLDIVNLFSLIRI-LANSND 295
      : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 13
AB3484
integral membrane protein [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanov
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3484
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAI5304.1; PID:g1798389; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11859
A:Map position: I
C:Superfamily: Escherichia coli ybhL protein

Query Match 10.7%; Score 136.5; DB 2; Length 245;
Best Local Similarity 29.1%; Pred. No. 5.3e-05;
Matches 64; Conservative 31; Mismatches 76; Indels 49; Gaps 10;
QY 55 AYHLILWN---IGGLITTMACMGSMVLLSAPPQE-----QKRVALLMA--AALF---- 100
      : : : : : : : : : : : : : : : : : : : : : :
Db 29 SYMLGVNMMATGLAVTGLAEGTAVLAQSNFAFQQLLPASPLRWIMLAPLAFAVFLSF 88
      : : : : : : : : : : : : : : : : : : : : : :
QY 101 --EGASIG-----PLIELGNFDPISIVFGAVGVCFAAAMARREYLY 148
      : : : : : : : : : : : : : : : : : : : : : :
Db 89 RIQSLSVGTAQAIFWGYAALVGLSL---SSIFVFTGQSVYRFEVTRASGALSLEY 144
      : : : : : : : : : : : : : : : : : : : : : :
QY 149 -----LGLLSGVSLLFWLHPAS--SIFGSMVAFKELYFGLLVFGYIVFTQDE 198
      : : : : : : : : : : : : : : : : : : : : : :
Db 145 TTKRNLSAMGSFLMMG--LFLGLILASVVNIFLGTALQFALSVGLIFAGLTAYTQDE 201
      : : : : : : : : : : : : : : : : : : : : : :
QY 199 IIEKAHLGD-----MDYVKHALTFTDFGAVFVRILLIM 232
      : : : : : : : : : : : : : : : : : : : : : :
Db 202 IKENYEGDAADTQGRKIVMGALRYLDLFINMFLLQPM 241
      : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
E81729
conserved hypothetical protein TC0206 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
C:Accession: E81729
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hicke
.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Saizbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A:Reference number: AB1500; MUID:20150255; PMID:10694935
A:Accession: E81729
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <TEU>
A:Cross-references: GB:AE002287; GB:AE002160; NID:g1790237; PIDN:AAF39078.1; PID:g719
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0206
C:Superfamily: Escherichia coli ybhL protein

Query Match 10.3%; Score 130.5; DB 2; Length 238;
Best Local Similarity 27.2%; Pred. No. 0.00018;
Matches 66; Conservative 35; Mismatches 95; Indels 47; Gaps 12;
QY 20 YDSLKNFQISPLVQTHLKQVY-----LTLCCALVASAAGY--LHILWNTGGLTFT 69
      : : : : : : : : : : : : : : : : : : : : : :
Db 4 YD--RDYTDQSRKLPQTFSRVYGNWMTAGLAVTALTSGLYATGAYRTLFSLW----WVWC 57
      : : : : : : : : : : : : : : : : : : : : : :

```

```
QY 70 MACMG-----SMWLLSAPPYQKRVALLMAAALFEGASIGPLIEL-GINFDPSIVFG 122
Db 58 FATLGVSFYIAQIQKLSVPV-----MGLFLAYSIVLEGMFTMPVYAAQFGGGVWA 112
QY 123 AFVGCNAVFCGFSNAAMLAR-----RREYLYLGLSSGVSLFLFWLHFASIFGGSMA 175
Db 113 AFGSAVIFGLSAAAYGAFTKSDTQIHRILMALIGLVV--ISLGF---LVVSLFTPMPL 167
QY 176 VKFELYFGLLVFGYIVFTQETIEKAHL-----GMDY---VKHALTLFTDFGAVFVRI 228
Db 168 MYLLICYLGLIIFVGLTVVDQAQSVRRVARSVGDHGLSYKLSLIMALQMYCNVIMIFWYL 227
QY 229 LII 231
Db 228 LQI 230

RESULT 15
E71467
Probable transport permease - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: E71467
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: E71467
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <ARN>
A:Cross-references: GB:AE001354; GB:AE001273; NID:g3329280; PIDN:AAC68416.1; PID:g332928
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: yccA
C:Superfamily: Escherichia coli ybhl protein

Query Match 10.1%; Score 128.5; DB 2; Length 238;
Best Local Similarity 25.9%; Pred.No. 0.00028;
Matches 63; Conservative 38; Mismatches 95; Indels 47; Gaps 12;

QY 20 YDSLKNFRQISPLVQTHLKOVY-----LTLCCALVASAAGAY--LHILWNIGGLTT 69
Db 4 YD--RDYQDSRLPGTFSSRVYGMTPAGLAVTALTSGLYATGAYRALFPW-----WINC 57
QY 70 MACMG-----SMWLLSAPPYQKRVALLMAAALFEGASIGPLIEL-GINFDPSIVFG 122
Db 58 FATLGVSFYIAQIQKLSVPV-----MGLFLAYSIVLEGMFTMPVYAAQFGGGVWA 112
QY 123 AFVGCNAVFCGFSNAAMLAR-----RREYLYLGLSSGVSLFLFWLHFASIFGGSMA 175
Db 113 AFGSAGIIFGLSAAAYGAFTKNDTQIHRILMALVGLV--ISLAFI---VSLFTPMPL 167
QY 176 VKFELYFGLLVFGYIVFTQETIEKAHL-----GMDY---VKHALTLFTDFGAVFVRI 228
Db 168 LYLICYLGLIIFVGLTVVDQAQSVRRVARSVGDHGLSYKLSLIMALQMYCNVIMIFWYL 227
QY 229 LII 231
Db 228 LQI 230
```

Search completed: September 22, 2003, 15:18:39
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:17:39 ; Search time 38 Seconds
(without alignments)
306.911 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272
Sequence: 1 MEGTSPFDSQASRRNSWY.....LIIMLNASKKPKKKRRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_Al:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023.5	80.5	247	1	BIL-ARATH
2	876.5	68.9	249	1	BIL-ORYSA
3	481.5	37.9	237	1	BIL-HUMAN
4	481.5	37.9	237	1	BIL-PAROL
5	479	37.7	236	1	BIL-RAT
6	312	24.5	245	1	BIL-DROME
7	165	13.0	345	1	GHIT-HUMAN
8	157.5	12.4	219	1	YCCA-ECOLI
9	143	11.2	297	1	YN45-YEAST
10	130.5	10.3	238	1	Y206-CHLMO
11	128.5	10.1	238	1	Y819-CHLTR
12	125.5	9.9	220	1	Y402-PASMU
13	124	9.7	231	1	Y893-DEIRA
14	123.5	9.7	231	1	Y236-CAMJE
15	122	9.6	234	1	Y8HL-ECOLI
16	121.5	9.6	239	1	Y52L-HCMVA
17	120	9.4	222	1	Y004-PSEAE
18	120	9.4	238	1	ZPRO-MOUSE
19	120	9.4	422	1	YF21-METJA
20	114.5	9.0	220	1	YCCA-HAEIN
21	114	9.0	227	1	Y420-NEIMA
22	113	8.9	223	1	Y058-VIBCH
23	112.5	8.8	230	1	Y920-HELPU
24	111	8.7	238	1	ZPRO-HUMAN
25	109.5	8.6	230	1	Y920-HELPU
26	108.5	8.5	236	1	Y147-RICPR
27	97	7.6	545	1	HGT1-CANAL
28	95	7.5	462	1	NHAC-BACFI
29	93.5	7.4	630	1	SSA4-CAVPO
30	93	7.3	234	1	YRJE-LACIA
31	92.5	7.3	229	1	Y358-STRPY
32	91	7.2	1124	1	TRPL-DROME
33	90	7.1	1094	1	EMBA-MYCTU

RESULT 1

ID	BIL-ARATH	STANDARD	PRT	247 AA
AC	Q9LD45			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Bax inhibitor-1 (BI-1) (AtBI-1).			
GN	BI-1 OR AT5G47120 OR K14A3.7.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
EX	MEDLINE=20086676; PubMed=10618494;			
RA	Kawai M., Pan L., Reed J.C., Ochiya H.;			
RT	"Evolutionally conserved plant homologue of the Bax inhibitor-1 (BI-1)			
RT	gene capable of suppressing Bax-induced cell death in yeast.";			
RL	FEBS Lett. 464:143-147(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia; TISSUE=Leaf;			
EX	MEDLINE=2024035; PubMed=10758491;			
RA	Sanchez P., de Torres Zabala M., Grant M.;			
RT	"AtBI-1, a plant homologue of Bax inhibitor-1, suppresses Bax-induced			
RT	cell death in yeast and is rapidly upregulated during wounding and			
RT	pathogen challenge.";			
RL	Plant J. 21:393-399(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RA	Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.;			
RT	Tabata S.;			
RL	"Structural analysis of Arabidopsis thaliana chromosome 5. XI.;"			
CC	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: SUPPRESSOR OF APOPTOSIS.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-!- SIMILARITY: BELONGS TO THE BIL FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; AB025927; BAA89541.2; -			
DR	EMBL; AF208124; AAG35727.1; -			
DR	EMBL; AB025609; BAA98107.1; -			
DR	PIR; T52449; T52449.			
DR	InterPro; IPR006213; Bax_inhbt1.			
DR	InterPro; IPR006214; UPF0005.			

Q9a2a3 caulobacter
O47479 loligo blee
O9cdm7 lactococcus
O29470 archaeoglob
Q9bbp6 lotus japon
Q9evn4 pseudomonas
O51489 borrelia bu
P47562 mycoplasma
P28008 staphylococ
Q95919 polyterus
P19845 pseudomonas
P45064 haemophilus

ALIGNMENTS

[illegible]


```

Db      129 TLSALYARRRSYFLGILMSALSLL--LSSLGNVFFSGTWLFQANLYGLIVMCGFVL 187
               : :|: |||| |::|||: | ||| | :|: |: |: |::| |::| |::| |::| |
Qy      195 DTQEITEKAHLGDMDYVKHALTITFDGFAGVFVRILIIMLNKASKEKKKKR 246
               ||| |||| | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: |
Db      188 DTQLITEKAHGDDYIWHCIDLDFDITVERKLMMILAMN--EKDKKKKK 237
               ||| |||| | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: |

RESULT 4
BIL_PAROL STANDARD; PRT; 237 AA.
ID ID BIL_PAROL
AC Q9IA79;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Probable Bax inhibitor-1 (BI-1).
OS Paralichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectesidae; Paralichthyidae; Paralichthys.
OC NCBI_TaxID=8255;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC TISSUE=Liver;
RA Lee J., Jeon J., Song Y.;
RT "Liver cDNA from Japanese flounder with similarity to TRGT.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -|- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
CC -|- SIMILARITY: BELONGS TO THE BI1 FAMILY.
-----
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-----
DR EMBL; AF220548; AAP61067.1; -.
DR InterPro; IPR006213; Bax_inhbt1.
DR InterPro; IPR006214; UPF0005.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; Bi1; 1.
KW Apoptosis; transmembrane.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 113 133 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
FT TRANSMEM 173 193 POTENTIAL.
SQ SEQUENCE 237 AA; 26570 MW; 344181AA386AB9A6 CRC64;

Query Match 37.98; Score 481.5; DB 1; Length 237;
Best Local Similarity 41.38; Pred. No. 4.1e-32;
Matches 95; Conservative 53; Mismatches 77; Indels 5; Gaps 3;

Qy      19 SYDSLKNFRDISPLVQPHKVLTICCALVASAAGAYLHTLWNI--GGLLTTMACMSG 76
               ::||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
Db      9 NFPSLKFSQISHSITQVHLKNYSVSLAVCFVAAGSYHVHVTFLFGGMLSVLGSLGM 68
               :||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |

Qy      77 VWLLSAP--PYEQKRVALMAAALPEGASIGPLIELGINFDPISIVEFGAVGCVVFGCF 134
               : :|: |||| |::|||: | ||| | :|: |: |: |::| |::| |::| |::| |::| |
Db      69 FWLAMTPHNSETBKRLAILAGFAFLTGVGLCPTLDFAVINPINSIIVTAFLGTSVIEWCF 128
               ||| |||| | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: |

Qy      135 SAAMLAARREYLVLGCLLSGSVSLFWLHFASFIFGSMVAKFKELYFLGLLVFGVIYF 194
               : :|: |||| |::|||: | ||| | :|: |: |: |::| |::| |::| |::| |::| |
Db      129 TLSALYAKRRSYFLGGLTMSGLSILFLMSNMNF--GSVMFLFAHYLGLLTMCGFVLX 187
               : :|: |||| |::|||: | ||| | :|: |: |: |::| |::| |::| |::| |::| |
Qy      195 DTQEITEKAHLGDMDYVKHALTITFDGFAGVFVRILIIMLNKASKEKKKK 244
               ||| |||| | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: |

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DB 188 DTQLIIIEKAENGDKDYVHWSVDLFDLFTIIPRKLMLVIALNDKDKKKEK 237

RESULT 5

```

BIL_RAT
ID BIL_RAT STANDARD; PRT; 236 AA.
AC P55062; Q64712;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).
GN TECT OR BIL
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=94281747; PubMed=8012111;
RA Walter L., Dirks B., Rothermel E., Heyens M., Szpirer C., Levan G.,
RA Guenther E.;
RT "A novel, conserved gene of the rat that is developmentally regulated
in the testis."
RL Mamm. Genome 5:216-221(1994).
CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH BCL2 AND BCL-XL (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
CC
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CC
CC EMBL; X75855; CAA53470.1; -
CC EMBL; X75856; CAA53471.1; -
CC FIC; S42069; S42069.
CC InterPro; IPR006213; Bax_inhbr1.
CC IntronPro; IPR006214; UPF0005.
CC Pfam; PF01027; UPF0005.1.
CC PROSITE; PS01243; BIL; 1.
CC
CC Apoptosis; Transmembrane.
FT TRANSMEM 30 50
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 88 108 POTENTIAL.
FT TRANSMEM 112 132 POTENTIAL.
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 206 226 POTENTIAL.
SQ SEQUENCE 236 AA; 26358 MW; FFA412EC1DCB7537 CRC64;

Query Match
Best Local Similarity 37.7%; Score 479; DB 1; Length 236;
Matches 100; Conservative 52; Mismatches 72; Indels 8; Gaps 5;

QY 19 SYDLKFNFRQISPLVQTHLKVYLLTCCALVASAAGAYHLIWN1--GGLLTTMACMGSM 76
DB 9 NFDALLKFSHTPTQOHLKKVYASFCALCMFAAGAVHVVTFTIQAGLLSALCALM 68
QY 77 VLLLSAPPYQ--EOKRVALLMAALFEGASTGLIELGINFDPSTVFGAVGCVVFCF 134
DB 69 ICLMATPSHETEQKRLGLL-AVAFLTGVLGPALELCIAINPSILPTAFMGTAIFTCF 127
QY 135 SAAAMLARRRYLYIGLLSSVSLFLWLFHFASTFGSMVAFKFLYFGLLVFGYIVF 194
DB 128 SLRAYRRYLYFGGLISAMS LMF--VSSGLNFIWFOANLYMGLLVCMGCVYLF 186
QY 195 DTQEIIEKAHLGDMYVVKHALTLFTDFGAVFVRILLIMKNASEKEKKKKR 246

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DB 187 DTQLIIIEKAENGDKDYIWHICIDLEDFVTLFRKLMLIAFN--EKDKKKEK 236

RESULT 6

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BIL_DROME
ID BIL_DROME STANDARD; PRT; 245 AA.
AC Q9VSH3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable Bax inhibitor-1 (BI-1).
GN CG7188.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.C., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abille J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley; TISSUE=Head;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacle J.M., Park S., Wan K.H.,
RA Rubin G.M., Celisner S.E.;
RT "A Drosophila full-length cDNA resource."
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
CC
CC -----

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QY 36 HLKQVYTLCCALYASAGAYLH--ILWNI---GGLLT---TMACMGSMWLLSAPPYQE 87
D 125 HSTWYLAGSGLTALSALISRTGPTVLMNFMWGRGSWVTIGVTEAAWVGAGMLVRSIPYDQ 184
QY 88 Q---KRVALLMAALFEGASTGPIELGINDPSIVFGAFVGCVAVFCFSAAAMLARR 144
D 185 SPGPKHLAWLHSGVM--GAVVAPLITLG---GPLLIRAAWYTAGIV--GGLSTVAMCAPSE 239
QY 145 EYLYGLGLSSGVSLLEWLHFPASSIFGSM-----AVFKFELFGLLVFVGYIVF 194
D 240 KFLNNGAPLVGLGLV-----FVSSL--GSMELPPTVAGATLYSVAMYGGLVLSFMELLY 293
QY 195 DTQETIEIKAHLDGM-----DYVKHALFLTFDFGAVFVRILIIIMLKNASEKE 240
D 294 DTQVKIKRAEVSPLYGVQKYPINSMLSIYMDTLNFMRVATMLATGNGNRKK 345

RESULT 8
YCCA_ECOLI
AC P06967;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein ycca.
GN YCCA OR B0970 OR C1110.
OS Escherichia coli, and
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236106; PubMed=6376117;
RA Tamura F., Nishimura S., Ohki M.;
RT "The E. coli d1ve mutation, which differentially inhibits synthesis
of certain proteins, is in trnSerL.";
RL EMBO J. 3:1103-1107(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Iano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=06:HI / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

```

```

CC -! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -! SIMILARITY: BELONGS TO THE BII FAMILY. STRONG, TO H-INFLUENZAE
CC HI0044.
CC -----
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CC -----
CC EMBL: X0547; CAA25218.1; -.
DR EMBL: AE000199; AAC74056.1; -.
DR EMBL: D90734; BAA35735.1; -.
DR EMBL: AE016758; AAN79578.1; -.
DR PIR: S07180; S07180.
DR EcoGene: EG11113; ycca.
DR InterPro: IPR006213; Bax_inhbr1.
DR InterPro: IPR006214; UPF0005.
DR Pfam: PF01027; UPF0005; 1.
DR PROSITE: PS01243; BII; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 23 43 POTENTIAL.
FT TRANSMEM 44 64 POTENTIAL.
FT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT TRANSMEM 158 178 POTENTIAL.
FT TRANSMEM 196 216 POTENTIAL.
SQ SEQUENCE 219 AA; 23362 MW; 4F787B853042ACD8 CRC64;

Query Match 12.4%; Score 157.5; DB 1; Length 219;
Best Local Similarity 27.0%; Pred. No. 5.7e-06;
Matches 65; Conservative 46; Mismatches 77; Indels 53; Gaps 12;

QY 12 SASRNRWSYDSLKNFRQISPLVOTH--LKQVY--LTLCALVASAAGAVLHILWNGIL 67
D 6 SSSHDRTS-----LLSTHKVLRNYFLLSLILAFSAITATATASTVLMLEPGLI 53
QY 68 TTMACMGSMWLLSAPPYQ--EQKRVALLMAAL--FEGASIGPLIELGINDF--PSIVFGA 123
D 54 LTLVGMYGLMFL---TYKTANKPTGIISAFATGTFGLVILPILNTVLSAGMGDVIA 109
QY 124 FVGCVAVFCFSAAAMLARRREYLYLGLLSGVSLF-----WLHPASSIFG 171
D 110 LGGTALVFFCCS--AYVLTRKDMSEFLGMLMAGIVVVLIGMVANIFLOLPALHLAIS--- 165
QY 172 GSMAYFKFELYFGLLVFVGYIVFDQETIEIKAHLDGMDYVKHALTLTFDFGAVFVRILII 231
D 166 ---AVF-----ILISSGAILFETSNII---HGGETNVRATVSLYVSLYVLSLII 212
QY 232 M 232
D 213 L 213

RESULT 9
YN45_YEAST
ID YN45_YEAST STANDARD; PRT: 297 AA.
AC P48558;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 33.6 kDa protein in MCK1-RPS19B intergenic region.
GN YNL305C OR N0405.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / FY1679;

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RX MEDLINE-96132033; PubMed-8553702;
RA Maurer K.C.T., Urbanus J.H.M., Planta R.J.;
RT "Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV
RT carrying a ribosomal protein gene cluster, the genes encoding a
RT plasma membrane protein and a subunit of replication factor C, and a
RT novel putative serine/threonine protein kinase gene.";
RL Yeast J1303-1310(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC
CC EMBL; U23084; AAC49093.1; -
CC EMBL; Z71581; CAA96233.1; -
CC PIR; S63281; S63281.
CC SGD; S0005249; YNL305C.
CC InterPro; IPR006214; UPF0005.
CC Pfam; PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 86 106 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
FT TRANSMEM 172 192 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 271 291 POTENTIAL.
FT TRANSMEM 297 297 AA; 33645 MW; 330784DAI17152B0 CRC64;
SQ SEQUENCE 297 AA; 33645 MW; 330784DAI17152B0 CRC64;

Query Match 11.2%; Score 143; DB 1; Length 297;
Best Local Similarity 24.3%; Pred. No. 0.00011;
Matches 65; Conservative 44; Mismatches 83; Indels 76; Gaps 13;
QY 31 PLV-QTHLKQVYLTCALVASAAGAY-----LHI-LWNTGGLTTWACMGS 75
DB 44 PIIRQRFHKVYSLSCOLLASLFCYWASVSTLQNFIMSHIALFYCMVSVLVC--- 100
QY 76 MVWLLSAP-----PYQSKR-----VALLMAALFECA 103
DB 101 -IWLAVSPEDYEASVPEPLTGSSEPAQQRRLPWVLSYKOKLTLISFTLSAY 159
QY 104 SIGPLIELGPNDFPSIVFGAFVGCFAAAMARREYLYLGLLSGVSILFLWL 163
DB 160 CLS-LVTLA--YDKDTVLSALLTITVVGVSVLTALSER-----FENVLSNATSIIYWL 210
QY 164 HF-----ASSIFGSMVAFKELYFGLL---VFVGYIVFTQEIIEKAHLGDMDY 210
DB 211 NWGLMIMTGMGTALLFGWNTSHSSFNLYGLWGLAILEFTAYLFDITQIFRKVY--PDDE 268
QY 211 VKHALTLFTDFGAVFVRIILMKNAE 238
DB 269 VRCAMMILYDIVNLFSLIIRI-LANSND 295

RESULT 10
Y206_CHLMU
ID Y206_CHLMU STANDARD; PRT; 238 AA.
AC O9PLA1.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TC0206.
GN TC0206.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nig9;

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RX MEDLINE-20150255; PubMed-10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Otterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
CC
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CC
CC EMBL; AE002287; AAF39078.1; -
CC TIGR; TC0206; -
CC InterPro; IPR006214; UPF0005.
CC Pfam; PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 49 69 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 238 238 AA; 26309 MW; 4625BID8093657E CRC64;
SQ SEQUENCE 238 AA; 26309 MW; 4625BID8093657E CRC64;

Query Match 10.3%; Score 130.5; DB 1; Length 238;
Best Local Similarity 27.2%; Pred. No. 0.00094;
Matches 66; Conservative 35; Mismatches 95; Indels 47; Gaps 12;
QY 20 YDLXNFKGISPLVOTHLKQVY-----LTLCCALVASAAGAY--LHILWNIGGLTT 69
DB 4 YD--RDYQDSRLPGLTFSRVYGVWTAGLAVTALSLGIYATGAYRTFLSL--WWWC 57
QY 70 MACMG-----SMWLLSAPPYQEQKRVALLMAALFEGASIGPLIEL-GINFDFSIYFG 122
DB 58 FATLGVSVFIQAQIQKLSVPAV-----MGLFLAYSVLGEMFGTVMVPVYAAQFGGIVWA 112
QY 123 AFVGCNAVVGCCFAAAMLAR-----RREYLYLGLLSGVSLLFLWLHFASIFGGSMA 175
DB 113 AFGSAVIFGLSAAAYGAFTKSDLTQTHRLMLALIGLV--ISLGF---LVVSLFTPMPL 167
QY 176 VFKEFLYFGLLVFGYIVFTQEIIEKAHL-----GDMY---VKHALTLFTDFGAVFVRI 228
DB 168 MYLLICYLGLIIFVGLTVVDAQSIRRVARSVGDHGLSVKLSLMLALQMYCNVIMFWYL 227
QY 229 LII 231
DB 228 LQI 230

RESULT 11
Y819_CHLTR
ID Y819_CHLTR STANDARD; PRT; 238 AA.
AC O84826;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein CT819.
GN CT819.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nig9;

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RP SEQUENCE FROM N.A.
 RC STRAIN=DJW-3/Cx;
 RX MEDLINE=99000809; PubMed=9784136;
 RA Stephens R.S., Kalman S., Lammell C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis";
 RL Sciense 282:754-759(1998).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE BIL FAMILY.
 CC
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 CC
 CC EMBL; AE001354; AAC68416.1; -
 CC PIR; E71467; E71467;
 CC InterPro; IPR006214; UPF0005.
 CC Pfam; PF01027; UPF0005; 1.
 CC
 CC Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 22 42 POTENTIAL.
 FT TRANSMEM 49 69 POTENTIAL.
 FT TRANSMEM 78 98 POTENTIAL.
 FT TRANSMEM 105 125 POTENTIAL.
 FT TRANSMEM 141 161 POTENTIAL.
 FT TRANSMEM 166 186 POTENTIAL.
 FT TRANSMEM 208 228 POTENTIAL.
 SQ SEQUENCE 238 AA; 26264 MW; FDI01F7B3867B8E5 CRC64;

Query Match 10.1%; Score 128.5; DB 1; Length 238;
 Best Local Similarity 25.9%; Pred. No. 0.0014;
 Matches 63; Conservative 38; Mismatches 95; Indels 47; Gaps 12;
 QY 20 YSLKNEQISPLVQTHLKQVY-----LTLCALVASAAGY--LHLWNIGGLTT 69
 DB 4 YD--RDYQDSRLPCTESSRVVGNMAGLAVTALTSGLYATGAYRALFPWM---WIWC 57
 QY 70 MACMG-----SMWLLSAPPYQOKRVALLMAALFGASIGPLIEL-GINFDPSIVFG 122
 DB 58 FATLGVSFYIAQIKLSVPV-----MGLFLAYSILEGMFFGLVPPVYAAQFGGGVYVA 112
 QY 123 AFVGCVVVFGCFSAAMLAR-----RREYLGLGLSSGVSLLFLHFASSIFGGSMA 175
 DB 113 AFGSAGIIFGLSAAYCAFTKNDLTQIHRILMLALVGLV--ISLAFLI---VSLFTPWL 167
 QY 176 VKFELVGLVGVGVYVDFDQEIIEKAHL-----GDMY---VKHALFTDFTDGFVVRKI 228
 DB 168 LYLICVGLLIIFVGLTVVDAQSIRRVARSVDGHDGLSKYLSLIMALQYCNVIMIFWYL 227
 QY 229 LII 231
 DB 228 LQI 230

RESULT 12
 Y402_PASMU STANDARD; PRT; 220 AA.
 AC Q9CNM5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein PM0402.
 GN PM0402.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Pm70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RA "Complete genome sequence of Pasteurella multocida Pm70";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE BIL FAMILY.
 CC
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 CC
 CC EMBL; AE006076; AAK02486.1; -
 CC InterPro; IPR006214; UPF0005.
 CC Pfam; PF01027; UPF0005; 1.
 CC
 CC Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 25 45 POTENTIAL.
 FT TRANSMEM 50 70 POTENTIAL.
 FT TRANSMEM 74 94 POTENTIAL.
 FT TRANSMEM 105 125 POTENTIAL.
 FT TRANSMEM 135 155 POTENTIAL.
 FT TRANSMEM 158 178 POTENTIAL.
 FT TRANSMEM 196 216 POTENTIAL.
 SQ SEQUENCE 220 AA; 23936 MW; 8EEC2E3FB4B5CDD5 CRC64;

Query Match 9.9%; Score 125.5; DB 1; Length 220;
 Best Local Similarity 25.4%; Pred. No. 0.0022;
 Matches 53; Conservative 44; Mismatches 93; Indels 19; Gaps 10;
 QY 32 LVQTH--LKQVYLTCCALVASAAGAYLHLWNI--GGLITMACMGSMWLLSAPPYQ- 86
 DB 14 LLNTHKVLNRYFYELGLTAFSAVVAYISMSLNLRPGILMLAGFYGLLEF---TYKL 69
 QY 87 EOKRVALLMAAL--FEGASIGPLIELGINDP-SIVEGAFVG-CAVVGCFSAAMLAR 142
 DB 70 SNSGLILSTFAFTGFLGYTLGPNLVVYSHGAGDIVVLAGTAGTAFFAC--SAYVLT 127
 QY 143 RREYLGLGLSSGVSLLFLHFASSIFGGSMAVFKFELYFGLLVGVYVDFDQEIIEK 202
 DB 138 KDMFSLGTIFALFIVLLMGVAFSTQSPMLYTAISGLFVVFVSTLG-ILYETSNII-- 184
 QY 203 AHLGDMYVKHALFTDFTDGFVVRILII 231
 DB 185 -HGGETNVIKATVSVFVSLYNLFISLLNI 212

RESULT 13
 Y893_DEIRA STANDARD; PRT; 231 AA.
 AC Q9RVX8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein DR0893.
 GN DR0893.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

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RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
CC -----
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CC -----
DR EMBL: AE001942; AAF10471.1; -
DR PIR: A75462; A75462.
DR TIGR: DR0893; -
DR InterPro: IPR006214; UPF0005.
DR Pfam: PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 26 46
FT TRANSMEM 56 76
FT TRANSMEM 84 104
FT TRANSMEM 112 132
FT TRANSMEM 142 162
FT TRANSMEM 163 183
FT TRANSMEM 206 226
FT TRANSMEM 231 AA; 24447 MW; BBB7D76A6445D9C9 CRC64;
SQ
Query Match 9.7%; Score 124; DB 1; Length 231;
Best Local Similarity 26.2%; Pred. No. 0.0031;
Matches 62; Conservative 41; Mismatches 94; Indels 40; Gaps 10;
QY 23 LKNEFQISPLVQTHLKQV-----YLLCCALVASAGAYL-----HILWNIGL-LTT 59
DB 2 VASQGIQIAWQTKTDQVTEFMARTYSWMAAGLUTAGVAYLTQAQGLAMQVASLRPL 61
QY 70 MACGMSVMWLLSAPPYQOKRVALLMAALFEG-ASIGPLI--ELGINFDPISVFGAFVG 126
DB 62 MLAQLALFVLS---MFAQRLSAAVAGALFVGYAALTGLTFSALLFAYSRAVITAFV 117
QY 127 CAVVFGCSAAMLARR-----RYLYIGLLSSGVSLFWLHPASSIFGSMVAFKFE 180
DB 118 SAGTEGLMSVAGFVKKDLSAMGRFFLF--AVYGLVWAMLV-----NLFVGSALSLSGI 169
QY 181 LYFGLLVGVXIVFQTEIEKHAHLG-----DMDYVKHALFTDFGAVFVRILII 231
DB 170 SMIGVFLFAGLTAYDTQMLRNLSGISGEQERASINGALALYLDIFNIFLFLNI 226
RESULT 14
Y236 CAMJE
ID Y236_CAMJE STANDARD; PRT; 231 AA.
AC Q9P1Q8.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical protein Cj0236c.
GN Cj0236C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCT 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
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CC -----
DR EMBL: AL139074; CAB72705.1; -
DR PIR: D81441; D81441.
DR InterPro: IPR006214; UPF0005.
DR Pfam: PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 36 56
FT TRANSMEM 58 78
FT TRANSMEM 83 103
FT TRANSMEM 143 163
FT TRANSMEM 170 190
FT TRANSMEM 231 AA; 25487 MW; 279E67CA380336C9 CRC64;
SQ
Query Match 9.7%; Score 123.5; DB 1; Length 231;
Best Local Similarity 26.8%; Pred. No. 0.0034;
Matches 62; Conservative 38; Mismatches 100; Indels 31; Gaps 10;
QY 20 YDSLKNEFQI-SPLVQTHLKQVYLTICCALVASAGAYLHIL---WNIGLLITMACMG 74
DB 8 YSRKEFEENTRSSELISIFIKQYQLFAASLLAATVGVGVIFALASFFIQSQVTEWILFA 67
QY 75 SMWLLSAPPYQOKRVALLMAALF-----EGASIGPLI--ELGINFDPISVFGAFVGC 127
DB 68 VEIGLIFA--LQKKREAPLNVLVLFGETFCGSLTLPILLISVLALPAGGIITAAQAFALT 125
QY 128 AVVFGCSAAMLARRREYLYLGG-----LISSGVSLFWLHPASSIFGSMVAFKFEIY 182
DB 126 TVAFAGLSVFM-NTKKDTVMGKALFVLIIVIVASLLNLFQSSIVNLAISA----- 178
QY 183 FGLLVFVGIVFDTQTEIEKHAHLGDMDY-VKHALTFTDFGAVFVRILIM 232
DB 179 VAAILFSFVLYDTONIIR---GNVETPIEGAVALYLDVNLVFSLLNIL 225
RESULT 15
YBHL_ECOLI
ID YBHL_ECOLI STANDARD; PRT; 234 AA.
AC P75768;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein ybhl.
GN YBHL OR B0786 OR C0868.
OS Escherichia coli, and
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]

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Job time : 40 secs

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SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba T., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takenoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
[3]
SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=2238234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-P., Boutin A., Hackett J., Stroud D.,
RA Maynew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -|- SIMILARITY: BELONGS TO THE BIL FAMILY.
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CC -----
DR EMBL; AE000181; AAC73873.1; -
DR EMBL; D90716; BAA35444.1; -
DR EMBL; AE016757; AAN79341.1; ALT_INIT.
DR PIR; B64815; B64815.
DR Ecogene; EG13668; YbHL.
DR InterPro; IPR006214; UPF0005.
DR Pfam; PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 24 44 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 80 100 POTENTIAL.
FT TRANSMEM 103 123 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT TRANSMEM 207 227 POTENTIAL.
SQ SEQUENCE 234 AA; 25902 MW; 7A59105563D5DFC8 CRC64;

Query Match 9.6%; Score 122; DB 1; Length 234;
Best Local Similarity 25.5%; Pred.No. 0.0045;
Matches 59; Conservative 41; Mismatches 81; Indels 50; Gaps 11;

QY 33 VQTHLKQVY-----LTLCALVSAAGAYLHILWN-----IGLLITMA---CMGSM 76
DB 17 LQTYNAQVYGVWTVGLLTFATFVAVTAANSAAVWELLFNVRVLIIGLIINQALVIVLSAM 76
QY 77 VMLLSAPPYQEQKRVALLMAALFEAGSTIGLIEGINFDPISVFCAVGCVAVFQCSA 136
DB 77 IQKLSA-----GVTTMLFMLSALTGLTSSIF---IVYTAASIATSEFVVTAGMFGAMSL 128
QY 137 AAMLARR-----REVLY---LGLLSSGVSLFLFHLFPASSIFGGSMVAFKFLYFGLIVF 188
DB 129 YGYTTKRDLSGFGNLMFLMAGLIGVILASLVN--FWLK-----SEALMWAVTYIGVIVF 178
QY 189 VGVIVFDTOEII---EKAHLGMDVYVKH-----ALTFTDFGAVFVRILII 231
DB 179 VGLTAYDTOKLNMGEQIDTQTSNLRKYSILGAULTLYLDIFNLFLMLRI 229
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Search completed: September 22, 2003, 15:20:27

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1134.5	89.2	249	10	Q93XB9	Q93xb9 nicotiana t
2	1027.5	80.8	247	10	Q8LAY4	Q8lay4 arabidopsis
3	1010.5	79.4	247	10	Q93XC0	Q93xc0 brassica na
4	1002.5	78.8	246	10	Q8W196	Q8w196 brassica ol
5	883	69.4	247	10	Q93XL2	Q93xl2 hordeum vul
6	523	41.1	146	10	Q8GT54	Q8gt54 hordeum vul
7	490.5	38.6	237	11	Q9D2C7	Q9d2c7 mus musculu
8	489.5	38.5	237	11	Q8BFY4	Q8bfy4 mus musculu
9	472	37.1	262	10	Q23599	Q23599 arabidopsis
10	435.5	34.2	187	10	Q9LTB6	Q9ltb6 arabidopsis
11	293	23.0	237	5	Q8IC41	Q8ic41 drosophila
12	238	18.7	334	5	Q8IKN3	Q8ikn3 plasmodium
13	192	15.1	305	5	Q9V1B2	Q9v1b2 drosophila
14	192	15.1	365	5	Q8T8Z4	Q8t8z4 drosophila
15	174.5	13.7	219	16	Q8Q061	Q8q061 salmonella
16	172	13.5	341	5	Q9VZ34	Q9vz34 drosophila

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QY 120 VGFAGVCAVFGCFSAAMARREYLILGGLSSGVLLFWLHFASIFGSGMAVFKF 179
DB 121 VIGAFVCAVAFGCFSAAMARREYLILGGLSSGVLLFWLHFASIFGSGMALFKF 180
QY 180 ELYFGLLVFGYIVFDQTQIEIKAHLGDMYVKHALTLFTDFGAVFVRILIMLKNASEK 239
DB 181 EYFGLLVFGYIVFDQTQIEIKAHLGDMYVKHALTLFTDFGAVFVRILIMLKNAADK 240
QY 240 EKKKKRRN 248
DB 241 EKKKKRRN 249

RESULT 2
Q8LAY4 PRELIMINARY; PRT; 247 AA.
AC Q8LAY4:
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Bax inhibitor-1 like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY087532; AAM65074.1; -.
DR InterPro; IPR006213; Bax_inhbt1.
DR InterPro; IPR001064; Crystallin.
DR PROSITE; PS01243; Btl; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY087532; AAM65074.1; -.
DR InterPro; IPR006213; Bax_inhbt1.
DR InterPro; IPR001064; Crystallin.
DR PROSITE; PS01243; Btl; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
SQ SEQUENCE 247 AA; 27455 MW; ABB31C674362F34 CRC64;

Query Match 80.8%; Score 1027.5; DB 10; Length 247;
Best Local Similarity 77.8%; Pred. No. 1.5e-81;
Matches 193; Conservative 31; Mismatches 23; Indels 1; Gaps 1;

QY 1 MEGFTSFDSQSASRNRSYSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 60
DB 1 MDAFSFFDSQPGSRS-WSYDSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 59
QY 61 WNIGLLTTCMCGSMWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEGINFDPISIV 120
DB 60 WNIGLLTTCMCGSMWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEGINFDPISIL 119
QY 121 FGAIFGCAVFGCFSAAMARREYLILGGLSSGVLLFWLHFASIFGSGMAVFKFE 180
DB 120 ITAFVGTATAFVCFSAAMARREYLILGGLSSGVLLFWLHFASIFGSGMAVFKFE 179
QY 181 LYFGLLVFGYIVFDQTQIEIKAHLGDMYVKHALTLFTDFGAVFVRILIMLKNASEK 240
DB 180 LYFGLLVFGYIVFDQTQIEIKAHLGDMYVKHALTLFTDFGAVFVRILIMLKNAADK 239
QY 241 EKKKKRRN 248
DB 240 EKKKKRRN 247

RESULT 3
Q93XC0 PRELIMINARY; PRT; 247 AA.
AC Q93XC0:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Bax inhibitor 1 (Bax inhibitor-like protein).
GN BI-1 OR Btl.
OS Brassica napus (Rape), and
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708, 3712;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.napus; STRAIN=cv. Westar; TISSUE=Leaf;
RA Boiduc N., Brisson L.;
RT "Characterization of Bax inhibitor 1 from Brassica napus.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.oleracea;
RA Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.;
RT "The isolation and characterization of broccoli homologs to
RT Arabidopsis PCD genes, LSD1 and B1: their role during cell death and
RT senescence.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF390555; AAK73101.1; -.
DR EMBL; AF453320; AAL50979.1; -.
DR InterPro; IPR006213; Bax_inhbt1.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR006214; UPF0005.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; Btl; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
SQ SEQUENCE 247 AA; 27526 MW; F5A5B5EFF64E8DB CRC64;

Query Match 79.4%; Score 1010.5; DB 10; Length 247;
Best Local Similarity 75.4%; Pred. No. 4.6e-80;
Matches 187; Conservative 35; Mismatches 25; Indels 1; Gaps 1;

QY 1 MEGFTSFDSQSASRNRSYSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 60
DB 1 MDSFSSFFDSQPGSRS-WSYDSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 59
QY 61 WNIGLLTTCMCGSMWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEGINFDPISIV 120
DB 60 WNIGLLTTCMCGSMWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEGINFDPISIL 119
QY 121 FGAIFGCAVFGCFSAAMARREYLILGGLSSGVLLFWLHFASIFGSGMAVFKFE 180
DB 120 ITAFVGTATAFVCFSAAMARREYLILGGLSSGVLLFWLHFASIFGSGMAVFKFE 179
QY 181 LYFGLLVFGYIVFDQTQIEIKAHLGDMYVKHALTLFTDFGAVFVRILIMLKNASEK 240
DB 180 LYFGLLVFGYIVFDQTQIEIKAHLGDMYVKHALTLFTDFGAVFVRILIMLKNAADK 239
QY 241 EKKKKRRN 248
DB 240 EKKKKRRN 247

RESULT 4
Q8W196 PRELIMINARY; PRT; 246 AA.
AC Q8W196:
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Bax inhibitor-like protein.
GN Btl.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Brassica.
OX	NCBI_TaxID=3712;
RP	[1]
RP	SEQUENCE FROM N.A.
RA	Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.;
RT	"The isolation and characterization of broccoli homologs to
RT	Arabidopsis PCD genes, LSD1 and BI: their role during cell death and
RL	senscence.";
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF453321; AAL50980.1; -.
DR	InterPro; IPR006213; Bax_inh1r1.
DR	InterPro; IPR001064; Crystallin.
DR	InterPro; IPR006214; UPF0005.
DR	Pfam; PF01027; UPF0005; 1.
DR	PROSITE; PS01243; B11; 1.
DR	PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
SQ	SEQUENCE 246 AA; 27375 MW; EBD0A01421B2DA2E CRC64;
QY	Query Match 78.8%; Score 1002.5; DB 10; Length 246;
Db	Best Local Similarity 76.0%; Pred. No. 2.2e-79;
Db	Matches 187; Conservative 33; Mismatches 25; Indels 1; Gaps 1
QY	1 MEGFTSFDDSSAGNRNWSYDLSKNFRQISPLVQTHLKQVYLFLCCALVASAAGAYLHL 60
Db	1 MESFSTFDDSPGSRSS-WSYESLKNLHQISVQNHLLKRVYLFLLCCALVASAFGAYLHVL 59
QY	61 WNIGGLLTMACMSWVLLSAPPYQOKRVALLMAALEFEGASIGFLIELGINEDPSIV 120
Db	60 WNIGGILITIAACCGTMIWLSCPPYEQOKRLSLFLFSAVLEGASVGLIKVAVDFDPSIL 119
QY	121 FGAFFGVCAVFCFSAAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMVAFKFE 180
Db	120 ITAFVGTALAFICFGAAMLARREYLYLGGLLSSGLSLMWLQFASSIFGGSASIFKFE 179
QY	181 LYFGLLVFGYIVDTQBIIEKAHLGDMYVKKHALTFTDFGAVFVRVLIIMLKNASEKE 240
Db	180 LYFGLLIEFVGWVVDTOBIIEKAHLGDMYVKKHALTFTDFVAVFVRVLIIMLKNASADKE 239
QY	241 EKKKKR 246
Db	240 EKKKER 245
RESULT 5	
Q93XL2	PRELIMINARY; PRG; 247 AA.
Q93XL2	
Q93XL2	Q93XL2; 01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	BAX inhibitor 1.
DE	PBI-1.
GN	Hordeum vulgare (Barley).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC	Triticeae; Hordeum.
OX	NCBI_TaxID=4513;
RP	[1]
RP	SEQUENCE FROM N.A.
RP	STRAIN=cv. Pallas;
RC	STRAIN=cv. Pallas; TISSUE=Leaf;
RA	Hueckelhoven R.;
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RP	STRAIN=cv. Pallas; TISSUE=Leaf;
RC	Hueckelhoven R., Dechert C., Trujillo M., Kogel K.H.;
RT	"Expression analysis of putative cell death regulator genes in near-
RT	isogenic, resistant and susceptible barley lines inoculated with the
RT	powdery mildew fungus.";
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AJ290421; CAC37797.1; -.
DR	InterPro; IPR006214; UPF0005.

DR	Pfam; PF01027; UPF0005; 1.
SQ	SEQUENCE 247 AA; 26962 MW; 4DBDFEFLEFAE22CC4 CRC64;
Query Match	69.4%; Score 883; DB 10; Length 247;
Best Local Similarity	67.1%; Pred. No. 5.e-69;
Matches 164; Conservative	36; Mismatches 42; Indels 0; Gaps 0;
QY	6 SPTDSGASRRNSYSOLKNFROIISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNIGG 65
Db	3 AFTYSTSAAASGWGHDSLKNFRQISPAVQSHLKLVLTLCFCALASSAVGAYLHIALNIGG 62
QY	66 LLTTMACGSMWLLSAPPYOQKRVALLMAAALFEFEGASIGPLTELGINFDPSIVFGAFV 125
Db	63 MLTFLACVGTIAMWFSPVVEERKRGGLMGAALEGASVGPLIELAIDFDP SILVTGFV 122
QY	126 GCADVFCFSAAAMLARRRXYLYLGSLSSGVSLLFWHFPASSIFGSGMAVFKEFYVL 185
Db	123 GTAIAGCFCSGAATIAKRRELYLGGLSLSSLGSLTLMLQLFVTSIFGHSSGSFMFEVYFVL 182
QY	186 LVPGVGYIVDTQETIEKAHLGDMVDYVKHALTLFTDGFAGVFRILLIMLNASEEKKKK 245
Db	183 LIFLGMVIDYTQELIERAHHGMDMYIKHALTLFTDFVAVLVRVLIIMLNAGDKSEDKK 242
QY	246 RR 247
Db	243 RK 244
RESULT 6	
ID Q8GT54	PRELIMINARY; PRT; 146 AA.
AC Q8GT54;	
DT 01-MAR-2003 (TREMBLrel. 23, Created)	
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE Putative BAX inhibitor 1 (fragment).	
GN PBI-1.	
OS Hordeum vulgare (Barley).	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;	
OX Triticeae; Hordeum.	
OC NCBI_TaxID=4513;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=cv. Pallas; TISSUE=Primary leaf;	
RA Hueckelhoven R., Kogel K.H.;	
RT "A BAX inhibitor 1 homologue is expressed differentially in barley	
RT primary leaves under pathogen attack.";	
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AJ278816; CAC82183.1; -.	
FT NON_TER 1	
FT NON_TER 146	
SQ SEQUENCE 146 AA; 15347 MW; A63D88030B7EE696 CRC64;	
Query Match	41.1%; Score 523; DB 10; Length 146;
Best Local Similarity	67.1%; Pred. No. 6.3e-38;
Matches 98; Conservative	21; Mismatches 27; Indels 0; Gaps 0;
QY	10 QSASRRNSYSOLKNFROIISPLVQTHLKQVYLTLCCALVASAAGAYLHILWNIGGLTT 69
Db	1 TSSAAASGWGHDSLKNFRQISPAVQSHLKLVLTLCFCALASSAVGAYLHIALNIGGLTM 60
QY	70 MACGSMWLLSAPPYOQKRVALLMAAALFEFEGASIGPLTELGINFDPSIVFGAFVGC 129
Db	61 LACYGTIAMWFSPVVEERKRGGLMGAALEGASVGPLIELAIDFDP SILVTGFVGT 120
QY	130 VFCFSAAAMLARRRXYLYLGSLSS 155
Db	121 AFCFSGNAITAKRRELYLYLGSLSS 146
RESULT 7	
99D2C7	

Query Match	38.5%	Score	489.5;	DB	11;	Length	237;
Best Local Similarity	43.1%;	Pred.	No. 8.6e-35;				
Matches	100;	Conservative	52;	Mismatches	73;	Indels	7;
Gaps							

QY	19	SYDSLKNFRQISPLVQTHLKVYLTLCCALVASAAGAYLHLWNI--GGLITTMACMGSM	134
Db	9	NFDALLKFSHIPTSQOHLKKYYASFALCMFVAAGAAYVVHTFIQAGLLSALGSLSALM	168
		: : : - - : : : : : : : : : : : : : :	
QY	77	VLLSSAPPYQ--EQRKVALLMRAALFEASGTGPLIEGINEDPSIVFGAFVGCAVFGCF	134
Db	69	IWLMPATPHSHETEQRKLGLAGFAIYLVGGGLPALELCIAVNPSILTFATFMGTAMITCF	128
		: : : : : : : : : : : : : : : : : :	
QY	135	SAAAMLARRELYLYLGSLSSGVSLFLWLHFASSIFGGSGMAVFPELYFGLLVFGVIYF	194
Db	129	SLSALYARRSYFLGLGIILMSAMSIML-LSSLGNLFPGSIWLFQANLYGLLLVMCGEVLF	194
		: : : : : : : : : : : : : : : : : :	
QY	195	DTQEITEKAHGLDMYVKALILFLDFDGAVFVRILLIMLKNASEEKKKKR	246
Db	188	DTQLITEKAHGDKDYIHCVDLFDFTVLFRKMLLIILAFN-EKDKKKEKK	237
		: : : : : : : : : : : : : : : : : :	

RESULT	9
O23599	PRELIMINARY;
ID	O23599
AC	O23599; PRT; 262 AA.
DT	01-JAN-1998 (TREMBLrel. 05, Created)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	Hypothetical 29.3 kDa protein (TEGT protein homolog).
GN	Atg17580.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX	NCBI TaxID=3702;

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 29.3 kDa protein (TEGR protein homolog).
GN Ar4G17580.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI TaxID=3702;

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RN  SEQUENCE FROM N.A.
RP  MEDLINE=98121113; PubMed=9461215;
RX  Bevan M., Bancroft J., Bent E., Love K., Goodman H., Dean C.,
RA  Bergkamp R., Dirksen W., van Staveren M., Stiekema W., Drost L.,
RA  Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
RA  Wedley E., Wambutt R., Weitzenecker T., Pohl T.M., Terryn N.,
RA  Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA  Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kottler P.,
RA  Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
RA  Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,
RA  Vouklatou E., Milioni D., Hatzipoulos P., Piravandi E., Obermaier B.,
RA  Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA  Palme K., Benes V., Rechman S., Ansoorge W., Cooke R., Berger C.,
RA  Delsenly M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,
RA  Schueller C., Chalwatzis N.;
RT  "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
RT  Arabidopsis thaliana.";
RL  Nature 391:485-488(1998).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  EU Arabidopsis sequencing project;
RL  Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR  EMBL; 297343; CAB78761.1; -
DR  EMBL; AL161546; CAB78761.1; -
DR  InterPro; IPR006213; Bax_inhbr1.
DR  InterPro; IPR006214; UPF0005.
DR  Pfam; PF01027; UPF0005; 1.
DR  PROSITE; PS01243; B11; 1.
SQ  SEQUENCE 262 AA; 29337 MW; 04111B60CE90F24F CRC64;

Query Match 37.1%; Score 472; DB 10; Length 262;
Best Local Similarity 61.7%; Pred. No. 3.2e-33;
Matches 95; Conservative 22; Mismatches 37; Indels 0; Gaps 0;

QY 87 EKKRYALLMAALFEGASIGPLIEGINFDPISIVFGAVGCGFSAAMLAARREY 146
DB 94 EAKRLYLFLFALLKGASVGMIMLVIDFSSVLVTAFTVGTAVFCFSAAMLAARREY 153
QY 147 LYLGLSSGVSLLFLWLFASIFGSGMAVFKFLYFGLLVFGYIVFTQBIIEKAHLG 206
DB 154 LYHGASLACCSILMWVQIASSIFGSGTVYKFKFLYFGLLVFGYIVFTQBIIEKAHLG 213
QY 207 DMDYVKHALFTDPAVGVFRILILMLKNASKE 240
DB 214 DMDYVQHSFTFTFDPAFLVQVILVNLMLILEKK 247

RESULT 10
Q9LVB6 ID Q9LVB6 PRELIMINARY; PRT; 187 AA.
AC Q9LVB6
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similarity to Bax inhibitor-1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB023609; BAA98108.1; -
DR InterPro; IPR006213; Bax_inhbr1.
DR PROSITE; PS01243; B11; 1.
SQ SEQUENCE 187 AA; 20867 MW; 876978A70592CF1E CRC64;

Query Match 34.2%; Score 435.5; DB 10; Length 187;
Best Local Similarity 50.0%; Pred. No. 3.3e-30;
Matches 96; Conservative 32; Mismatches 47; Indels 17; Gaps 4;

QY 62 NTGGLLTLMACGSMV-WLLSAPPYQEOKRVALLMAALFEGASIGPLIEGINFDPISIV 120
DB 4 NTGGITITKLGVLSLLEHVSCPYPYKHKIRFSLLLFGLVHGASVGPCKISTIDISLIL 63
QY 121 FGAIVGCAVFGCFSAAMLAARREYLYLGLLSGVSLFLWL---HFASIFGSGMAV 176
DB 64 ITAFICGTAVIFCFSAAMLAARREYLYLGLLSGVSLFLWLKNSDOPAS-----AT 116
QY 177 KFELYFGLLVFGYIVFTQBIIEKAHLGDMYVKHALFTDPAVGVFRILILMLKNA 236
DB 117 VEIQMYLGLLVFGYIVFTQBIIEKAHLGDMYVAVHSLILYIGVFRVFLQILSILMNWTS 176
QY 237 SEKEKKKKRRN 248
DB 177 AD-----RIRN 183

RESULT 11
Q8IQAL ID Q8IQAL PRELIMINARY; PRT; 237 AA.
AC Q8IQAL;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CG7188-PB.
GN CG7188.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobaraj C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner T.C., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Sidenkiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of *Drosophila melanogaster*."
 RN Science 287:2185-2195(2000).
 RP [2]
 RN SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzone J., An H., Baldwin D., Bantz J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champagne M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ilegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragad V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RL "Sequencing of *Drosophila melanogaster* genome."
 RP Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RL "Annotation of *Drosophila melanogaster* genome."
 RP Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RA FlyBase:
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003556; AAN12018.1; -.
 SQ SEQUENCE 237 AA; 26468 MW; E5F54AA6DBAA84A6 CRC64;

Query Match 33.0%; Score 293; DB 5; Length 237;
 Best Local Similarity 24.4%; Pred. No. 1e-17;
 Matches 72; Conservative 44; Mismatches 81; Indels 12; Gaps 4;

QY 31 PLVQTHLKQVLTCCALVASAGAYLHI--LWNTGGLLTMACMGSMVWLLSAPPYQEQ 88
 DB 25 PYVREHLSKVYVGLGSTAAATAMGAMQMRDFLDLG----VLAAVATLVVLGLHFYKDD 80
 QY 89 -----KRVALLMAALFFEGASIGPLIELGINFDPISIVFGAFVGCFSAAAMLARR 143
 DB 81 GKNYTRIGMLYAFGFCGSLGILGLGYICSINPAIILSALTGTFTFISLSLALLAEQ 140
 QY 144 REYLYLGGLLSGVSLLEFWLHPASSIFGSGMAVFKFELYGLLVFGVIVPDTQEIIEKA 203
 DB 141 GKLYLGGMLVSVINTMALLSLFNMFV-KSYEVQVQTLVGVGVMAAFIVYDTONIVEKC 199
 QY 204 HLGDMYVYKHALTFTDFGAEVFRILIM 232
 DB 200 RGNRDVVVOHALDLDFVLSMFRLLIIL 228

RESULT 12
 Q81KN3 PRELIMINARY; PRT; 334 AA.
 AC Q81KN3;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN PF14_0571.
 OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3D7;
 RX MEDLINE=22255705; PubMed=12368864;
 RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
 RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.;
 RL "Genome sequence of the human malaria parasite *Plasmodium falciparum*."
 RT Nature 419:498-511(2002).
 RL EMBL; AE014825; AAN37184.1; -.
 KW Hypothetical protein.
 DR SEQUENCE 334 AA; 39849 MW; 62E1138B99BA140D CRC64;

Query Match 18.7%; Score 238; DB 5; Length 334;
 Best Local Similarity 28.7%; Pred. No. 9e-13;
 Matches 75; Conservative 52; Mismatches 108; Indels 26; Gaps 9;

QY 4 FTSPF-----DSQASRNRSYDSLKNFRQISPLV---QTHLKQVLTCCALVASAA 53
 DB 81 FTNIFGYNIEKMDPLNQIKKQRIINLSNMFSPLENEERHLLKIYGLLAGTIVSAL 140
 QY 54 GAYLHLW-NIGGLTLMACMGSMVWLLSA--PPYQ--EOKRVALLMAALFFEGASIGPL 108
 DB 141 SCYVDIVYKVPREIASIISLVCSFLLSSCNSHYQLVDTSKRLVYVFAGI--SSSIGVL 198
 QY 109 IELGINF----DPSIVFGAFVGCFSAAAMLARRREYLYLGGLLSGVSLFWLH 164
 DB 199 ISDYINYVYVNLNPSILPLAFFGSLIFCCSLAATFSKNRISIFLGAVLCVCSYMALIS 258
 QY 165 PASSIFGSGMAVFKFELYGLLVFGVIVPDTQETIEKAHLGDMYVYKHALTFTDFGAV 224
 DB 259 F-MNFFIRSKEDITLTLYTGFFMYGFLVDTQITLDFRGNKDYIMHSICLYLDLVL 317
 QY 225 FVRILIMKNASKEKEKKK 245
 DB 318 FTHLLRL---GQKEKEKKK 334

RESULT 13
 Q9VIB2 PRELIMINARY; PRT; 305 AA.
 AC Q9VIB2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE CG1287 protein.
 GN CG1287.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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RESULT 15
ID Q82Q61
ID Q82Q61 PRELIMINARY; PRG: 219 AA.
AC Q82Q61;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative TEGT family carrier/transport protein.
DE YCCA OR STM1085
GN YCCA
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
[1]
FN SEQUENCE FROM N.A.
RP STRAIN=Lt2 / SGSC1412 / ATCC 700720;
RC MEDLINE=15134948; Pubmed=11677609;
EX McClelland M., Hubbard K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium

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RL  Nature 415:852-856(2001).
DR  EMLL; AE008747; AAL20018.1; -.
DR  InterPro; IPR006213; Bax_inhbt1.
DR  InterPro; IPR006214; UPF0005.
DR  Pfam; PF01027; UPF0005.1.
DR  PROSITE; PS01243; B11; 1.
DR  KW Hypothetical protein; Complete proteome.
SQ  SEQUENCE 219 AA; 23313 MW; 9FA28BACE70B8497 CRC64;
      Query Match      13.7%; Score 174.5; DB 16; Length 219;
      Best Local Similarity 29.6%; Pred. No. 1.9e-07;
      Matches 67; Conservative 42; Mismatches 76; Indels 41; Gaps 11;
QY  27  RQISPLVQTH--LKQVY--LTLCALVASAGAYLHLWNIGLLTWTMACGSMVWLISA 82
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   9  RDRSLSLTHKVLRTVFLSLTALSAITASTVLMPSGILTLVGMGLMFL--- 65
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  83  PPYQ-EOKRVALLMAAL--PEGASIGPLIEIGINFDF-SIVFG-AFVGCADVFCFAAA 138
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db      66 -TYKTANKPVGILSAPAFITGLIIPILINAYLSAGMGDVIGLALGTALVFPCCS-AY 123
QY      139 MLARREPREYIAGLISSGVSLF-----WLHFASSIFGSSMAVFKFELYGGL 186
Db      124 VLTTRKDMSPFGMLAGIYVVLIGVANIFLOPALHLAIS-----AVF-----IL 170
QY      187 VFVGYIVFDIOELIEKAHLGMDYKHAJLFTFDGAVFVRILIM 232
Db      171 ISSGAILIYETSNI---HGGETNYIRATVSLYVSLYNIYFVLSIL 213
  
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Search completed: September 22, 2003, 15:21:52
 Job time : 74 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 22, 2003, 15:23:18 ; Search time 2813 Seconds
(without alignments)
3606.679 Million cell updates/sec

Title: US-09-955-526-4
Perfect score: 1272
Sequence: 1 MEGFSPFDSDSASRRMSY.....LIIMLNKASEKEKKKKRRN 248

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -GPMT=fastap -SUFFIX=rgc -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Diosum62 -TRANS=human40.cdi -LIST=45
-DOCLIN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09955526.rcgn.1.1.5265.0runat.22092003.151754.12365 -NCPU=6 -ICPU=3
-NO_MMAP -LARGOUDRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -YGAPOP=6
-YGAPEXT=7 -ZGAPOP=10 -ZGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl :
1: gb_da : *
2: gb_hgt : *
3: gb_in : *
4: gb_om : *
5: gb_ov : *
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7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_ro : *
11: gb_sts : *
12: gb_sy : *
13: gb_un : *
14: gb_vi : *
15: em_da : *
16: em_fun : *
17: em_hum : *
18: em_in : *
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20: em_om : *
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23: em_pat : *
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25: em_pl : *
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27: em_sts : *
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29: em_vi : *
30: em_htg_hum : *
31: em_htg_inv : *
32: em_htg_other : *
33: em_htg_mus : *
34: em_htg_pln : *
35: em_htg_rtd : *
36: em_htg_mam : *
37: em_htg_vrt : *
38: em_sy : *
39: em_htgo_hum : *
40: em_htgo_mus : *
41: em_htgo_other : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1134.5	89.2	1293	AF390556	AF390556 Nicotiana
2	1027.5	80.8	1066	AY087532	AY087532 Arabidops
3	1023.5	80.5	775	AY114059	AY114059 Arabidops
4	1023.5	80.5	994	AY091134	AY091134 Arabidops
5	1023.5	80.5	1006	AF208124	AF208124 Arabidops
6	1023.5	80.5	1117	AB025927	AB025927 Arabidops
7	1010.5	79.4	1010	AF390555	AF390555 Brassica
8	1010.5	79.4	1013	AF453320	AF453320 Brassica
9	1002.5	78.8	1019	AF453321	AF453321 Brassica
10	883	69.4	744	HVU290421	HVU290421 Hordeum v
11	876.5	68.9	750	AX660456	AX660456 Sequence
12	876.5	68.9	1181	AB025926	AB025926 Oryza sat
13	811	63.8	1137	AX660801	AX660801 Sequence
14	810	63.7	1137	AX660802	AX660802 Sequence
15	786.5	61.8	750	AB025607	AB025607 Sequence
16	767	60.3	34498	AB025609	AB025609 Arabidops
17	688.5	54.1	884	AR231128	AR231128 Sequence
18	523	41.1	438	HVU278816	HVU278816 Hordeum v
19	512	40.3	198788	ATCHRIV46	ATCHRIV46 Arabidops
20	512	40.3	207674	ATFC48	ATFC48 Arabidops
21	499.5	39.3	527	AR231129	AR231129 Sequence
22	492.5	38.7	2331	BC005588	BC005588 Mus muscu
23	483.5	38.0	892	AF033095	AF033095 Homo sapi
24	483.5	38.0	2609	BC000916	BC000916 Homo sapi
25	483.5	38.0	2695	BC036203	BC036203 Homo sapi
26	482.5	37.9	1745	AF220548	AF220548 Paraliich
27	481	37.8	940	RNTEGT2	RNTEGT2 Sequence
28	479.5	37.7	2634	AR058920	AR058920 Sequence
29	479.5	37.7	2634	AR058921	AR058921 Sequence
30	479.5	37.7	2634	AR112791	AR112791 Sequence
31	479.5	37.7	2634	AR112792	AR112792 Sequence
32	478.5	37.7	2634	AR305046	AR305046 Sequence
33	479.5	37.7	2634	AR305047	AR305047 Sequence
34	479.5	37.7	896	RNTEGT3	RNTEGT3 Sequence
35	473.5	37.2	2600	HSTEGT	HSTEGT Sequence
36	470	36.9	418	G73645	G73645 R.sapiens T
37	468	36.8	127507	AP005311	AP005311 Oryza sat
38	468	36.8	155492	AP005304	AP005304 Oryza sat
39	464.5	36.5	3339	BC047131	BC047131 Xenopus l
40	340	26.7	360	G71526	G71526 A61521534FM
41	312	24.5	1102	AY058377	AY058377 Drosophil
42	305	24.0	520	BD058151	BD058151 Secreted
43	272.5	21.4	380	BD027963	BD027963 Sequence
44	269	21.1	110032	AC014916	AC014916 Drosophil
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RESULT 1

ALIGNMENTS

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LOCUS AF390556 1293 bp mRNA linear PLN 28-JAN-2003
DEFINITION Nicotiana tabacum Bax inhibitor 1 (BI-1) mRNA, complete cds.
ACCESSION AF390556
VERSION AF390556.1 GI:14719275
KEYWORDS
SOURCE
ORGANISM Nicotiana tabacum (common tobacco)
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; Lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS 1 (bases 1 to 1293)
TITLE Bolduc, N., Ouellet, M., Pitre, F. and Brisson, L.F.
Molecular characterization of two plant BI-1 homologues which
suppress Bax-induced apoptosis in human 293 cells
JOURNAL Planta 216 (3), 377-386 (2003)
MEDLINE 22408492
PUBMED 12520328
REFERENCE 2 (bases 1 to 1293)
AUTHORS Bolduc, N., Pitre, F. and Brisson, L.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2001) Biochemistry and Microbiology, Laval
University, Quebec G1K 7P4, Canada
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Location/Qualifiers
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/db_xref="GI:14719275"
/translation="MESCISFNSQSSSRNRKNSYSLKRNQISPEVQHLKKVYLS
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GASIGPLIEAIDEDPSIVIGAFVGAFCGCAAMVARRREYLVIGLISGLSI
LFWLHPASSTIGSGMALPKFVRYGLIVPGYIIFEDQDIENKHLDDLYKNAIIL
FTDPAVAVFRLITMLKNSDKERKKRRR"
BASE COUNT 296 a 243 c 304 g 450 t
ORIGIN
Alignment Scores:
Pred. No.: 8.9e-106 Length: 1293
Score: 1134.50 Matches: 217
Percent Similarity: 95.58% Conservative: 21
Best Local Similarity: 87.15% Mismatches: 10
Query Match: 89.19% Indels: 1
DB: 8 Gaps: 1
US-09-955-526-4 (1-248) x AF390556 (1-1293)
QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAla----SerArgAsnArgTyrPser 19
DB 134 ATGGAGTCTTGACATCTCTTCATTCACAGTCGGCGTCTCGCAATCGCTGGAGT 193
QY 20 TyrAspSerLeuYsAsnPhaArgGlnIleSerProLeuValGlnThrHisLeuYsGln 39
DB 194 TACGATTTCTTAAACATCTCCGCGAGATCTCTCTTGTTCACACTCATCTCAAAAG 253
QY 40 ValTyrIleThrLeuYsCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisTle 59
DB 254 GTCTACCTTCATATATGTTGCTTACTGCTTGGCTGCTGGAGCTTACTTCACATT 313
QY 60 LeuTrrpanIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrrpLeu 79
DB 314 CTTCGAGCAATGGGCTTACTTACGACATTCGATTCGAGCAATGATGATGCTGCTG 373
QY 80 LeuSerAlaProTrrGlnGlnGlnYsArgValAlaLeuLeuMetAlaAlaLeu 99

DB 374 ATGGCGACACCTCTGATGAAAGACAAAGATACACCTCTGATGCGACGTCAGT 433
QY 100 PheGlnIleYsAlaSerIleGlyProLeuIleGlnLeuIleYsPheAspProSerIle 119
DB 434 TTTAAAGACATCTTATTTGCTTCCATGTAATGACTTATGACTTGGACCCAGCAT 493
QY 120 ValPheGlyAlaPheValGlyCysAlaValAlaValPheGlyCysPheSerAlaAlaIleMet 139
DB 494 GTGATCGGTGCTTTGTTGTTGCTGCTGCTGCTTTGTTGCTGCTGCTGCTGCTG 553
QY 140 LeuAlaArgArgArgGlyTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeu 159
DB 554 GTGCAAGCGCGACAGAGACTTGTATCTGAGAGCTCTTCTTATCATGCTGCTCTATC 613
QY 160 LeuPheThrLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheYsPhe 179
DB 614 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
QY 180 GluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnIle 199
DB 674 GAGTTTATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 733
QY 200 IleGlnYsAlaHisLeuGlyAspMetAspTyrValYsHisAlaLeuThrLeuPheThr 219
DB 734 ATTGAGAGGCGACACCTTGGGATTTGACTACGTGAGCATGCTGACCTCTTACA 793
QY 220 AspPheGlyAlaValAlaPheValArgIleLeuIleIleMetLeuYsAsnAlaSerGluYs 239
DB 794 GATTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 853
QY 240 GluGlnYs 248
DB 854 GAG 880
RESULT 2
LOCUS AY087532 1066 bp mRNA linear PLN 14-APR-2003
DEFINITION Arabidopsis thaliana clone 36400 mRNA, complete sequence.
ACCESSION AY087532
VERSION AY087532.1 GI:21406269
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS Haas, B.J., Volkovskiy, N., Town, C.D., Troukhan, M., Alexandrov, N.,
Feidmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE 22088475
PUBMED 12093376
REFERENCE 2 (bases 1 to 1066)
AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feidmann, K.
TITLE Full-length cDNA from Arabidopsis thaliana
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1066)
AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feidmann, K.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to fRGC and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of
the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants; including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have

[illegible]

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Query Match:	75.40%	Mismatches:	25
	79.44%	Indels:	1
	8	Gaps:	1
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QY 1	MetGluglyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTyrSerTyr	20	
DB 38	ATGATTCATCTCTGCTCTCTCTCTGATTCCTACACCTGGTAGCAGAA--TGGAGCTAT	94	
QY 21	AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal	40	
DB 95	GATTCTCTCAAAAACCTCCGTCAGATTTCTCCCTCCGTCAGAAATCATCTCAAGGGGTT	154	
QY 41	TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaIaGlyAlaTyrLeuHisIleLeu	60	
DB 155	TATCCATCTCTGTGTGTGTCTCTGTCCTGTCCTGGTTGGAGCTTACTCTCAGCTGCTC	214	
QY 61	TrpAsnIleGlyGlyLeuLeuThrThrmethIaCysMetGlySerMetValTrpLeuLeu	80	
DB 215	TGGAAACATAGGTGGTATTTCTCACAACCTTGGATGGCTTTGAGAGCATGATGGCTGCTC	274	
QY 81	SerAlaProPOTyrGlnGlnGlnLysArgValAlaLeuLeuMetAlaAlaAlaLeuPhe	100	
DB 275	TCGTCCTCTCTTATGACAAACAAAGAGGCTTTCCTCTCTGTCTCTGCTGCTCTC	334	
QY 101	GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal	120	
DB 335	GAAAGTCCTGATGGTGTGCTTGTATCAAGAGCGAGATTGATTTGACCCAAAGCATTCCTC	394	
QY 121	PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaIaMetLeu	140	
DB 395	ATCAGTCGGTTTGTGGAACTGCGATTCCTTATCTGTCTCTCAGGGGCGACGATGTG	454	
QY 141	AlaArgArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu	160	
DB 455	GCAAGACGACAGAGATACCTGCTACCTCGAGAGAGACTGTTCACTGGCTTGGCATGCTT	514	
QY 161	PheTrpPheHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu	180	
DB 515	ATGTGGCTTCAGTTTGCCCTCTTCACATCTTGGTGGCTCTGCATTCATCTTTAAGTTTGA	574	
QY 181	LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnIuIleIle	200	
DB 575	CTCTACTTTGAGACTTTGATCTTTTGGATATCATGTGTGGACACTCATCATATTTATA	634	
QY 201	GluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAsp	220	
DB 635	GGAAGAGGCCACCTCGTGACATGGATTACGGAACATTCCTTACCCCTTTTCCACCGAT	694	
QY 221	PheGlyAlaValPheValArgIleLeuIleIleMetLeuLysAsnAlaSerGlnLysGlu	240	
DB 695	TTTGTAGCTGTGTGTGTGTGTGTGTCTCATCATTTTGTCTAAGAAACTCGGCAATTAAGA	754	
QY 241	GluLysLysLysLysArgArgAsn 248		
DB 755	GATAAAAAGAGAGAGGAGGAAC 778		
LOCUS AF453320	1013 bp	mRNA	linear
DEFINITION Brassica oleracea bax inhibitor-like protein (Bil)			mRNA, complete cds.
ACCESSION AF453320			
VERSION AF453320.1	GI:17981373		
KEYWORDS	Brassica oleracea		
SOURCE	Brassica oleracea		
ORGANISM			

BASE COUNT	246 a	228 c	220 g	325 t			
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Alignment Scores:							
Pred. No.:	1,71e-92	Length: 1019					
Score:	1002.50	Matches: 187					
Percent Similarity:	89.43%	Conservative: 33					
Best local Similarity:	76.02%	Mismatches: 25					
Query Match:	78.81%	Indels: 1					
DB:	8	Gaps: 1					
US-09-955-526-4 (1-248) x AF453321 (1-1019)							
QY	1 MetLunglyPheThrIrrSerPhePheAspSerGlnSerAlaSerAlaArgAsnArgTyr 20						
DB	54 ATGGAACGCTGTCTGCTCCCTTCCTGATTCCTACGACGCGACGCAAGC---TGGAGCTAT 110						
QY	21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40						
DB	111 GAATCTCTCAAGAAGCCCTCAGATCTCCCGCCGCTACAGAAATCATGCTCAAGCGGCT 170						
QY	41 TyrIleuThrLeuLysCysAlaIleValAlaSerAlaIleValAlaGlyAlaTyrLeuHisIleLeu 60						
DB	171 TATCTCACTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 230						
QY	61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValIrrPheLeu 80						
DB	231 TGGAAACATCGGTGATATTCACACACATTCGATGCTGGAACACATGATTTGGCTTCTC 290						
QY	81 SerAlaProPyrIrrGlnGlnGlnLysArgValAlaLeuLeuMetAlaIleAlaLeuPhe 100						
DB	291 TCATGTCCTCTCTTATGAGCAACAAAGAGGCTCTCATCTCTCTCTCTCTCTCTCTCTCT 350						
QY	101 GlnGlyAlaSerIleGlyProLeuIleGlnLeuGlyIleAsnPheAspProSerIleVal 120						
DB	351 GAAAGTGTCTGTGTGGCCCTTATCATAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 410						
QY	121 PheGlyAlaPheValIleGlyCysAlaValAlaPheGlyCysPheSerAlaIleAlaMetLeu 140						
DB	411 ATCATCGGTGTTGTCGGAACGTGCATAGCGCTTATGCTTCTCTCTCTCTCTCTCTCTCT 470						
QY	141 AlaArgAlaArgGlnTyrLeuTyrLeuGlyIleLeuLeuSerSerGlyValSerLeuLeu 160						
DB	471 GCCAGACGCCAAGAGGTATCTCTACCTCGGAGGAGCTTCTCTCTCTCTCTCTCTCTCTCT 530						
QY	161 PheIrrPheuHisPheAlaSerSerIlePheGlyIleSerMetAlaValPheLysPheGln 180						
DB	531 ATGTGGCTTCAGTTGTTGCTCTTCATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 590						
QY	181 LeuTyrPheGlyLeuLeuValPheValIleTyrIleValPheAspThrGlnIleIle 200						
DB	591 CTCACACTTGGACCTGTGATCTTTGTTGGATACATGAGTGGGACACACAGACATATATA 650						
QY	201 GlnLysAlaHisIleGlnLysPheMetAspTyrValLysHisAlaLeuThrLeuPheThrAsp 220						
DB	651 GAGAAAGACACACCTCAGGGGACATGACATATGTGAACATGCATATGACCCCTTTACCCGAT 710						
QY	221 PheGlyAlaValPheValArgIleLeuIleIleMetLeuLysAsnAlaSerGlnLysGln 240						
DB	711 TTGTGGCTGT 770						
QY	241 GlnLysLysLysLysArg 246						
DB	771 GAGAAAGAAAGAGAGAGA 788						
RESULT 10							
LOCUS	HVU290421	744 bp	mRNA	linear PLN 18-JAN-2002			
DEFINITION	Herdum valigare mRNA for BAX inhibitor 1 (pBI-1 gene).						
ACCESSION	AJ290421						
VERSION	AJ290421.1	GI:13940164					
KEYWORDS	BAX inhibitor 1; pBI-1 gene.						

[illegible]

Bunkuo-ku, Tokyo 113-0032, Japan
(E-mail: uchimiya@imcbs.iam.u-tokyo.ac.jp, Tel: 81-3-3812-2910,
Fax: 81-3-3812-2910)

On Mar 8, 2000 this sequence version replaced gi:6759252.
Sequence updated (02-Mar-2000).

FEATURES

Source

1. .1181
/organism="Oryza sativa"
/mol_type="mRNA"
/strain="Yamahoushi"
/db_xref="taxon:4530"
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126. 875
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/codon_start=1
/product="Box inhibitor-1"
/protein_id="BAA89540.3"
/db_xref="GI:7209772"
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ASVPLIKLAVDESSILYAFVGTALATGCTCAALVAKRREYLVLGLISGLSIL
LWLOFAASIFGHTSGEMFEYFGLIFIGYVYDQEIIEERAHGDMYIKHALILF
TDFVAVILRVILMLKNASDKSEKKRKRKRS"
BASE COUNT 262 a 295 c 317 g 307 t
ORIGIN

Alignment Scores:

Pred. No.: 1.27e-79 Length: 1181
Score: 876.50 Matches: 165
Percent Similarity: 82.33% Conservative: 40
Best Local Similarity: 66.27% Mismatches: 43
Query Match: 68.91% Indels: 1
DB: 8 Gaps: 1

US-09-955-526-4 (1-248) x AB025926 (1-1181)

QY 1 MetGluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTirpSerTyr 20
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QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
DB 186 GACTCGCTGAAGAACTTCGCGCAGATCTCCCGCGCTCCAGTCCACCTCAAGCTCGTT 245
QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaGlyAlaTyrLeuHisIleLeu 60
DB 246 TACCTGACACATGATGCTCGCTCGCTGGCGGGTGGCGCATACCTGCACGTCGCC 305
QY 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
DB 306 TTGAACATCGGGGATCTTGACTATGCTGGGTGCTGGGAGCATCGCTGGTGTTC 365
QY 81 SerAlaProProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
DB 366 TCGGTGCTGCTTTTGAAGAGAGAGAGAGAGTGTGGGATCTCTTGGCGCTCCCTGCTG 425
QY 101 GlnGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
DB 426 GAAGGGCTTCAGTTGGGCTCTGATCAAGCTGCTGTAGATCTTGACCTCAAGCATCTC 485
QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeu 140
DB 486 GTAACAGCATTTGTTGAACTGCCATTCATTCATTTGGGTGCTTCACCTGCGCTGCACT 545
QY 141 AlaArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeu 160
DB 546 GCCAAGCGTAGGAGTACCTCTACCTTGGTGGTGTCTCTCTCTGGCTCTCCATCTCTG 605
QY 161 PheTrpLeuHisPheAlaSerIlePheGlySerMetAlaValPheLysPheGlu 180
DB 606 CTCTGGCTGAGTTTGGCGCATCCATCTTTGGCCACTCCACCGGAGCTTCATGTTTGA 665

QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleLeu 200
DB 666 GTTACTTTGGCTGTGTAICTTCTGGGTACATGGTGTATGACACGAGGAGATCAT 725
QY 201 GlnLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAsp 220
DB 726 GAGAGGGCTCACCACGGTGACATGGACTACATCAAGCAGCGACTCACCTCTTCACTGAC 785
QY 221 PheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGluLys--- 239
DB 786 TTCTGGTGGCGTCTCTTCTGGGATCTTCGTCATCATGCTCAAGAACCGGCTGACAACTCG 845
QY 240 GlnGluLysLysLysLysArgArgAsn 248
DB 846 GAGGAGAAGAAGAGAGAGAGAGGTCT 872
RESULT 13
AX660801
LOCUS 1137 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1158 from Patent WO03000906.
ACCESSION AX660801
VERSION AX660801.1 GI:29162565
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE 1
AUTHORS Glazebrook, J., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,
Katagiri, F., Kreps, J., Provart, N., Riecke, D. and Zhu, T.
TITLE Plant disease resistance genes
JOURNAL Patent: WO 03000906-A 1158 03-JAN-2003;
SYNOPSIS Syngenta Participations AG (CH)
FEATURES
source 1. .1137
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/mol_type="genomic DNA"
/db_xref="taxon:4565"
BASE COUNT 224 a 318 c 324 g 271 t
ORIGIN
Alignment Scores:
Pred. No.: 5.47e-73 Length: 1137
Score: 811.00 Matches: 165
Percent Similarity: 79.76% Conservative: 36
Best Local Similarity: 65.48% Mismatches: 45
Query Match: 63.76% Indels: 6
DB: 6 Gaps: 0
US-09-955-526-4 (1-248) x AX660801 (1-1137)
QY 2 GluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTirpSerTyrAsp 21
DB 99 CAGGAGATGACGCCCTTCTACTCGCTCGTGGCGGCGGAGGATGGGGCTACGAC 158
QY 22 SerLeu-LysAsnPhe-ArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 41
DB 159 TCGCTTCAAGAACTTCGGGGAGATCTCCCGCGCTGCAAGCCCACTCAAGCTCGTT 218
QY 41 TrpLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyr--LeuHisIleLeu 60
DB 219 ACCCTGACCTATGCTTTGCCCTGGCTCATCTGCGTGGGTGCTTAACCTGCACATG 278
QY 60 euTrpAsnIleGlyLeuLeuThrThrMet-AlaCysMetGlySerMetValTrpLeu 79
DB 279 CCCTGAACATCGGTGGGATGCTGACAAATGCTTTGGTGTATCGGACCAATGCTCGCTG 338
QY 80 LeuSerAlaProProTyrGlnGluLysArgValAlaLeuLeuMetAlaAlaLeu 99
DB 339 TACTCTGCTGCTATGAGGAGAGAGAGAGTGGGGCTGCTGATGGGTGCGAGCCCTC 398
QY 100 PheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIle 119

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Db      399  CTGAAAGGGCTTCGGTGGACCTCTGATGAGCTTGCCATAGACCTTGACCAACGATC 458
QY      120  ValPheGlyAlaPheValGlyCysAlaValAlaValPheGlyCysPheSerAlaAlaMet 139
Db      459  CTGCTGACAGGTTTGTGCGAACGCCATCGCTTCGGGTGCCTCTGTCGCGCGGCATC 518
QY      140  LeuAlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeu 159
Db      519  ATGCCAAGCGCAGGAGTACCTGTACCTGGGGCCTGCTCTCTGCTGCTGCTGCTGCTGCT 578
QY      160  LeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPhe 179
Db      579  CTGCTCTGGTTCAGTTTGGCAGCTTGCACCTCACTTTGGCCACCTCTGCGCCTTCATGTT 638
QY      180  GluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluLeu 199
Db      639  GAGGTTTACCTTGGCTTGTGATCTCTCTGGGGTACATGACGACGACGACGACGACGATC 698
QY      200  IleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThr 219
Db      699  ATCAGAGGGCGCCACCGGTGACATGACATCAAGCAGCGGCTCACCCTCTTACC 758
QY      220  AspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGluLys 239
Db      759  GACTTCGTGCGCGCTCTCTCGCGATCTCATCATCATCATCATCATCATCATCATCATCAT 818
QY      240  GluGluLysLysLysLysArgArg 247
Db      819  TCGGAGGACAAGAGAGAGGAG 842

RESULT 14
AX660028
LOCUS      887 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION      Sequence 385 from Patent WO03000906.
ACCESSION      AX660028
VERSION      AX660028.1 GI:29162013
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
              Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS      Glazebrook,J., Briggs,S., Cooper,B., Goff,S.A., Moughamer,T.,
              Katagiri,F., Kreps,J., Provart,N., Ricke,D. and Zhu,T.
TITLE      Plant disease resistance genes
JOURNAL      Patent: WO 03000906-A 385 03-JAN-2003;
              Syngenta Participations AG (CH)
FEATURES
source      1..887
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              /mol_type="genomic DNA"
              /db_xref="taxon:4530"
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ORIGIN

Alignment Scores:
Pred. No.:      5.14e-73      Length:      887
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Best Local Similarity:      64.45%      Mismatches:      43
Query Match:      63.68%      Indels:      8
DB:      6      Gaps:      3

US-09-955-526-4 (1-248) x AX660028 (1-887)

QY      1  MetLluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
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QY      21  AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40

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Db      61  GACTCGCTGAAGAACTTCGCCAGATCTCCCGCGCGCTCCAGTCCACCTCAAGCTCGTT 120
QY      41  TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
Db      121  TACTGACACTATGCTGCCCTTGGCTGGCGGTGGCGCATACCTGCACGTCCGCG 180
QY      61  TrpAsnIleGlyGlyLeuLeuThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db      181  TTGAACATCGCGGGATGTTGACTATGCTCGGTGGTGGGGAGCATCGCGCTGGTGTTC 240
QY      81  SerAlaProProTyrGlnGlu-----Gln-LysArgValAlaLeuLeuMetAlaAla 98
Db      241  TCGGTGCTCTCTTTGAGGAGTAGACAGAGAGAGAGTTGGGATTCCTCTGCGCGTGC 300
QY      98  aLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAsp--Pro 117
Db      301  CCGCTCGAGGGGCTTCAGTTGGGCTCTGATCAAGCTTGTCTAGACTTGTACTCAAG 360
QY      118  SerIleValPheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAla 137
Db      361  AGCATTCTCGTACAGCATTTGTTGAACTGCCCATTTGGGTGCTTCACTTGGCT 420
QY      138  AlaMetLeuAlaArgArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyVal 157
Db      421  GCCATCGTTCAGAGCGTAGGAGTACCTCTACCTTGGTGGTTCCTCTCTCTGCGCTC 480
QY      158  SerLeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPhe 177
Db      481  TCCATCTCTGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY      178  LysPheGlu---LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThr 196
Db      541  ATGTTTGAGCAGGTTTACTTTGGCTGTGATCTTCCCTGGGTGATGTTGTTATGACAG 600
QY      197  GlnGluIleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThr 216
Db      601  CAGGAGATCATCGAGGGCTCACCAGGTGACATGACTACATCAAGCAGCAGCTCACC 660
QY      217  LeuPheThrAspPheGlyAlaValPheValArgIleLeuIleMet-LeuLysAsnAl 236
Db      661  CTCTTCACTGACTTCGTGGCGCTCTGTCGGATCTCTGTCGATCTGTCATGCTCAAGAACG 720
QY      236  aSerGluLys---GluGluLysLysLysLysArgArgAsn 248
Db      721  GTCTGACAAGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760

RESULT 15
AX660870
LOCUS      750 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION      Sequence 1227 from Patent WO03000906.
ACCESSION      AX660870
VERSION      AX660870.1 GI:29162634
KEYWORDS
SOURCE
ORGANISM      Zea mays
              Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
              clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS      Glazebrook,J., Briggs,S., Cooper,B., Goff,S.A., Moughamer,T.,
              Katagiri,F., Kreps,J., Provart,N., Ricke,D. and Zhu,T.
TITLE      Plant disease resistance genes
JOURNAL      Patent: WO 03000906-A 1227 03-JAN-2003;
              Syngenta Participations AG (CH)
FEATURES
source      1..750
              /organism="Zea mays"
              /mol_type="genomic DNA"
              /db_xref="taxon:4577"
BASE COUNT      130 a      233 c      200 g      187 t
ORIGIN

Alignment Scores:

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Pred. No.: 1.03e-70 Length: 750
Score: 786.50 Matches: 158
Percent Similarity: 78.69% Conservatives: 34
Best Local Similarity: 64.75% Mismatches: 45
Query Match: 61.83% Indels: 7
DB: Gaps: 3

US-09-955-526-4 (1-248) x AX660870 (1-750)

QY 11 GlnSerAlaSerArgAsnArg-----TrpSerTyrAspSerLeuLysAsnPheArg 27
DB 19 CAATCGCAGCGAGGAGGCGGCGCGCGCTTCGAATCGCTCAAGCGTCTGGGT 78

QY 28 GlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeuThrLeuCysCysAla 47
DB 79 CACATCTCACCGCGTGTGCGCTCCCAACATGTACCTCAACCTCAACCTCGAGGCGCGTTC 138

QY 48 LeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsnIleGlyLeuLeu 67
DB 139 CTGGCGCTTCTCGCATCTCGCGGTACCTCCATCTCTCAACCTCGAGGCGCGCTTC 198

QY 68 ThrThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProTyr----- 85
DB 199 ACGACGCGGTGGTGGTGGTCCATCGCTTCCTCATCTCCCTGCGCGCTTCACGGAC 258

QY 86 GlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPheGluGlyAlaSerIle 105
DB 259 CAGGAGAGGAACCGCTTGGCGTGTCTCATGTCTGCGCGCTCTTCAAGCGCGTCCGTT 318

QY 106 GlyProLeuIleGluLeuGlyLeuAsnPheAspProSerIleValPheGlyAlaPheVal 125
DB 319 GGTCCGCTCGTGCACCTGTTATGTGCTGATTCGAGATTCTCTCATCTGCGTTCGTC 378

QY 126 GlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeuAlaArgArgGlu 145
DB 379 GGGACCGCAGTTCCTTTGCATGCTTCTGGCGCTCCCATCATCGCCCAAGCGCGAGAA 438

QY 146 TyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeuPheTrpLeuHisPhe 165
DB 439 TACCTGTACCTCGCGGTCTGCTTTCATCTGCGCTCTCCATCTCTGCTGCTGCTGCTT 498

QY 166 AlaSerSerIlePheGlyGlySerMetAlaValPheIlePheGlyLeuTyrPheGlyLeu 185
DB 499 GCTACTTCAATCTTGGCCACACCGCGGACCTTCATGTTGAGCTCTACTTGGCCIC 558

QY 186 LeuValPheValGlyTyrIleValPheAspThrGlnGluIleIleGluLysAlaHisLeu 205
DB 559 CTGGTTTCTCGGATATATGTTGTTGACACCGAGAGATCATCGAGGGCGCACCGGT 618

QY 206 GlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAlaValPhe 225
DB 619 GGGGACATGACATACATCAAGCAGCGGTGACTCTCTTCAACGACTTGTGTGGGTCTT 678

QY 226 ValArgIleLeuIleIleMetLeuLysAsnAlaSerGluLys-----GluGluLysLys 243
DB 679 GTTCGATCTCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 738

QY 244 LysLysArgArg 247
DB 739 AGGAAGAAGCGG 750

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Search completed: September 22, 2003, 16:21:15
Job time : 2822 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 22, 2003, 15:21:58 : Search time 267 Seconds
(without alignments)
2507.343 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGFTSFDSQASNRWSY.....LIIMKNASEKEKKKRN 248

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	688.5	54.1	884	22	AAF44782	Testis Enhanced Ge
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5	492.5	38.7	712	21	AAC51940	Arabidopsis thaliana
6	491.5	38.6	873	22	AAF92293	Bovine mammary tis
7	483.5	38.0	2922	21	AAF18054	Lung cancer associ
8	483.5	38.0	2994	25	ABX63356	Human cDNA #356 di
9	479.5	37.7	2634	19	AAV59067	Bax inhibitor Bi-1
10	473.5	37.2	2600	24	ABK84658	Human cDNA differe
11	426	33.5	376	25	ABX19768	Human GDP-mannose
12	382.5	30.1	751	24	ABQ56073	Human ovarian anti
13	371.5	29.2	536	24	ABV88094	Human colon cancer
14	312	24.5	1085	23	ABL12505	Drosophila melanog
15	310.5	24.4	638	23	ABV23517	Human prostate exp
16	305	24.0	520	20	AAV86028	EST clone B115. H
17	296	23.3	251	25	ABX25165	Human GDP-mannose
18	285	22.4	410	25	ABX43279	Bovine EST associa
19	275.5	21.7	595	24	ABQ59227	Human colon cancer
20	272.5	21.4	380	21	AAC04218	Human secreted pro
21	269	21.1	375	23	ABL12504	Drosophila melanog
22	256.5	20.2	689	24	ABQ60318	Human colon cancer
23	255	20.0	257	25	ABX24245	Human GDP-mannose
24	219	17.2	392	25	ABX43548	Bovine EST associa
25	219	17.2	431	25	ABX48159	Bovine EST associa
26	192	15.1	1359	23	ABL02337	Drosophila melanog
27	192	15.1	3359	23	ABE02336	Drosophila melanog
28	191	15.0	463	21	AAC03759	Human secreted pro
29	188	14.8	601	21	AAA16226	Human colon cancer
30	172	13.5	1198	23	ABL03963	Drosophila melanog
31	171	13.4	2475	21	AAC86459	Mouse brown adipos
32	165	13.0	1035	21	AAZ48818	Human DERP2 coding
33	165	13.0	1038	25	ABZ75900	Heart disease targ
34	165	13.0	1268	21	AZA48819	Human DERP2 coding
35	165	13.0	1316	21	AAZ58548	Human haemopoietic
36	165	13.0	1355	24	ABK35731	cDNA sequence #122
37	165	13.0	1394	20	AAV73001	Human adult testis
38	165	13.0	1394	24	ABQ92026	Human polynucleoti
39	165	13.0	1429	25	ABZ75907	Heart disease targ
40	165	13.0	1596	19	AAV59684	Human secreted pro
41	165	13.0	1596	24	ABZ73671	Human cDNA #1 for
42	165	13.0	1714	20	AAZ77497	Human ovarian tumo
43	165	13.0	1943	21	AAZ64941	Membrane-bound pro
44	165	13.0	1943	22	AAF44087	Human PRO281 (UNQ2
45	165	13.0	1943	24	ABK69961	cDNA encoding huma

ALIGNMENTS

RESULT 1
ABN98455

ID ABN98455 standard; DNA; 1009 BP.

XX ABN98455;

AC ABN98455;

DT 01-AUG-2002 (first entry)

XX Arabidopsis thaliana expressed polynucleotide SEQ ID NO 223.

XX Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;

KW disease; crop; thale cress; tolerance factor; insect; pathogen;

KW nutrition; ds.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX US2002023281-A1.

FN

DT	17-OCT-2000	(first entry)
XX	XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 21973.
DE	XX	Hybridisation assay; genetic mapping; gene expression control;
KW	XX	protein identification; signal transduction pathway;
KW	XX	metabolic pathway; promoter; termination sequence; ss.
XX	XX	Arabidopsis thaliana.
OS	OS	Arabidopsis thaliana.
XX	XX	EP1033405-A2.
XX	XX	06-SEP-2000.
PD	XX	25-FEB-2000; 2000EP-0301439.
PF	XX	25-FEB-1999; 99US-0121825.
PF	XX	05-MAR-1999; 99US-0123180.
XX	XX	09-MAR-1999; 99US-0123548.
XX	XX	23-MAR-1999; 99US-0125788.
XX	XX	25-MAR-1999; 99US-0126264.
XX	XX	29-MAR-1999; 99US-0126785.
XX	XX	01-APR-1999; 99US-0127462.
XX	XX	06-APR-1999; 99US-0128234.
XX	XX	08-APR-1999; 99US-0128714.
XX	XX	16-APR-1999; 99US-0129845.
XX	XX	19-APR-1999; 99US-0130077.
XX	XX	21-APR-1999; 99US-0130449.
XX	XX	23-APR-1999; 99US-0130510.
XX	XX	23-APR-1999; 99US-0130891.
XX	XX	28-APR-1999; 99US-0131449.
XX	XX	30-APR-1999; 99US-0132048.
XX	XX	30-APR-1999; 99US-0132247.
XX	XX	04-MAY-1999; 99US-0132484.
XX	XX	05-MAY-1999; 99US-0132485.
XX	XX	06-MAY-1999; 99US-0132486.
XX	XX	06-MAY-1999; 99US-0132487.
XX	XX	07-MAY-1999; 99US-0132863.
XX	XX	11-MAY-1999; 99US-0134256.
XX	XX	14-MAY-1999; 99US-0134218.
XX	XX	14-MAY-1999; 99US-0134219.
XX	XX	14-MAY-1999; 99US-0134221.
XX	XX	14-MAY-1999; 99US-0134370.
XX	XX	18-MAY-1999; 99US-01343768.
XX	XX	19-MAY-1999; 99US-0134941.
XX	XX	20-MAY-1999; 99US-0135124.
XX	XX	21-MAY-1999; 99US-0135353.
XX	XX	24-MAY-1999; 99US-0135629.
XX	XX	25-MAY-1999; 99US-0136021.
XX	XX	27-MAY-1999; 99US-0136392.
XX	XX	28-MAY-1999; 99US-0136782.
XX	XX	01-JUN-1999; 99US-0137222.
XX	XX	03-JUN-1999; 99US-0137528.
XX	XX	04-JUN-1999; 99US-0137502.
XX	XX	07-JUN-1999; 99US-0137724.
XX	XX	08-JUN-1999; 99US-0138094.
XX	XX	10-JUN-1999; 99US-0138540.
XX	XX	10-JUN-1999; 99US-0138847.
XX	XX	14-JUN-1999; 99US-0139119.
XX	XX	16-JUN-1999; 99US-0139452.
XX	XX	16-JUN-1999; 99US-0139453.
XX	XX	17-JUN-1999; 99US-0139492.
XX	XX	18-JUN-1999; 99US-0139454.
XX	XX	18-JUN-1999; 99US-0139455.
XX	XX	18-JUN-1999; 99US-0139456.
XX	XX	18-JUN-1999; 99US-0139457.
XX	XX	18-JUN-1999; 99US-0139458.
XX	XX	18-JUN-1999; 99US-0139459.
XX	XX	18-JUN-1999; 99US-0139460.
XX	XX	18-JUN-1999; 99US-0139461.
XX	XX	18-JUN-1999; 99US-0139462.
XX	XX	18-JUN-1999; 99US-0139463.
XX	XX	18-JUN-1999; 99US-0139750.


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PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 10-SEP-1999; 99US-0152363.
PR 17-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 24-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0155659.
PR 29-SEP-1999; 99US-0156458.
PR 04-OCT-1999; 99US-0156596.
PR 05-OCT-1999; 99US-0157117.
PR 08-OCT-1999; 99US-0157863.
PR 07-OCT-1999; 99US-0158029.
PR 12-OCT-1999; 99US-0158232.
PR 13-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159284.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 4,71e-109
Score: 1004.50
Percent Similarity: 90.32%
Best Local Similarity: 77.82%
Query Match: 2
DB: 21

US-09-955-526-4 (1-248) x AAC38715 (1-1066)

QY 1 MetCluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
Db 49 ATGCATCGGTCTCTCTTCCTTCGATTCCTCAACCTGGTAGCAGAGC---TGGAGCTAT 105
QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
Db 106 GATTCCTTAAARACTTCGTCAGATTCCTCCAGCCGTTCCAGATCATCTTAACGGGTT 165
QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
Db 166 TATTGACCTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 225

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QY 61 TrpAsnIleGlyGlyLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 226 TGAATATCGCGGTATCTTACACGATTGGATGTATTGGAACATGATATTGGCTCCTT 285
QY 81 SerAlaProProTyrClnGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
Db 286 TCATGTCTCTCTTATGACACCAACCAAAAGGCTTCTCTCTCTGTCGCTGCTGTTCT 345
QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
Db 346 GAAGGTGCTTCTGTGGCCCTTGATCAGAATGGCAATTGATGTTGACCCAGCATCCTT 405
QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeu 140
Db 406 ATCACTGCGCTTGTGGAACTGCGATAAG-TTGTCTGTTCTCAGCAGCAGCAATGTTA 464
QY 141 AlaArgArgArgGlnTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
Db 465 GCAAGACGAGGAGTATCTTACCTTGAGGACTGCTTTCATCTGCTGCTGCTGCTGCTA 524
QY 161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180
Db 525 ATGTGCTCCAGTTTCCCTCTTCGATCTTTGGTGGCTGCTGCACTATCTTAAAGTTGAG 584
QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleLe 200
Db 585 TTGTACTTTGGACTTTTGATCTTTGCGGATACATGTAAGAACTTCGTGACCTTTTCACTGAC 644
QY 201 GluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAsp 220
Db 645 GAAAGGACACCTCGGTGACATGGACTATGTAAGAACTTCGTGACCTTTTCACTGAC 704
QY 221 PheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGluLysGlu 240
Db 705 TTGTAGCTGTGTTTGTGGATTCATCATATGTTGAAGAACTCAGCAGATAAGAA 764
QY 241 GluLysLysLysLysArgArgAsn 248
Db 765 GAGAGAAGAAGAAAGAGGAAAC 788

RESULT 3
AAF44782
ID AAF44782 standard; cDNA; 884 BP.
XX AC AAF44782;
XX DT 27-MAR-2001 (first entry)
XX DE Testis Enhanced Gene Transcript protein coding sequence #1.
XX KW Cell death modulator; programmed cell death; PCD; apoptosis;
XX KW forestry plant; ss.
XX OS Pinus radiata.
XX PN WO200075331-A1.
XX PD 14-DEC-2000.
XX PF 02-JUN-2000; 2000WO-N200086.
XX PR 04-JUN-1999; 99US-0325932.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX PI Flinn B, Lasham A;
XX DR WPI; 2001-061724/07.
XX DR P-PSDB; AAB65755.
XX PT Novel defender against cell death polynucleotide useful for modulating
programmed cell death pathway and specific development pathways in

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PT forestry plant -
XX
PS
PS
XX
XX
Claim 1; Page 62; 142pp; English.
XX
CC The present invention relates to coding sequences (see AAF44740-F44840
and AAF4843-F44844) and proteins (see AAB65714-B65814) involved in
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins
CC of the present invention are useful for modulating a PCD or cell death
CC pathway and various developmental pathways in a forestry plant, by
CC stably incorporating one of the present coding sequences into the genome
CC of the forestry plant, where the coding sequence provides a PCD pathway
CC that is not present in a native form of the forestry plant.
XX
SQ Sequence 884 BP; 219 A; 165 C; 216 G; 284 T; 0 other;
XX

Alignment Scores:
Pred. No.: 1,04e-71 Length: 884
Score: 688.50 Matches: 137
Percent Similarity: 79.25% Conservative: 31
Best Local Similarity: 64.62% Mismatches: 41
Query Match: 54.13% Indels: 3
DB: 22 Gaps: 2

US-09-955-526-4 (1-248) x AAF44782 (1-884)
QY 39 GlnValTyrLeuThrLeuThrLeuThrLeuThrLeuThrLeuThrLeuThrLeuHis 58
Db 2 AGGGTTATTGTCGCTTAGCTGTCCTCGTAACAGCAGCGATCGGTGTTTATGTCAT 61
QY 59 IleLeuTrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrp 78
Db 62 CTCTCTGTAATATTGGAGGGCTCCTCAGCGGGCTCGCTTGCATGCTGTCTGATCGGG 121
QY 79 LeuLeuSerAlaPro-----ProTyrGlnGluGlnLysArgValAlaLeuMetAla 96
Db 122 CTTCTACCGCTCCTACTCTCCGAAACATGAGGGTAAGAGAGCTCGCTGCTTCCTGGCA 181
QY 97 AlaAlaLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyLeuLeuSerPhe 116
Db 182 GCTGCTGCTGCTCAAGGGAGCTACTCTGGGACCGCTCATCGACGCGCTCATTAATATTGAC 241
QY 117 ProSerIleValPheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAla 136
Db 242 TCCAGTATATCTGTGAGTGCCTGTTGTTGGACCTCTTGGCCTTCGCTTTCGGCA 301
QY 137 AlaAlaMetLeuAlaArgArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGly 156
Db 302 GCAGCAATCACAGCCAGAGAGCGGGAATACCTATTGTTGGAGGATATTGGCTCGGGA 361
QY 157 ValSerLeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaVal 176
Db 362 ATCAGCATATTGATGTGGTGTCAACTAGCATCTCGATTTTGGTGGTCTTTCGGCGATT 421
QY 177 PheLysPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThr 196
Db 422 TACACATTGAGATCTACCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
QY 197 GlnGluIleLeuLysAlaHisLysLysAspMetAspTyrValLysHisAlaLeuThr 216
Db 482 CAGATCATCATCAGAAAGCGGACCATGGAGACTATGATATTATAAATCCTCCTGAGCA 541
QY 217 LeuPheThrAspPheGlyAlaValPheValArgIleLeuIleLeuMetLeuLysAsnAla 236
Db 542 CTCTTCATTGACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
QY 237 ---SerGluLysGluLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 247
Db 602 GACAGTAATATCCAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGG 637

RESULT 4
AAF44783
ID AAF44783 standard; cDNA; 527 BP.
XX

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AC AAF44783;
XX
DT 27-MAR-2001 (first entry)
XX
DE Testis Enhanced Gene Transcript protein coding sequence #2.
XX
KW Cell death modulator; programmed cell death; PCD; apoptosis;
KW forestry plant; ss.
XX
OS Pinus radiata.
XX
PN WC200075331-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-NZ00086.
XX
PR 04-JUN-1999; 99US-0325932.
XX
PA (GENF-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Flinn B, Lasham A;
XX
DR WPI; 2001-061724/07.
DR P-PSDB; AAB65756.
XX
PT Novel defender against cell death polynucleotide useful for modulating
PT programmed cell death pathway and specific development pathways in
PT forestry plant -
XX
XX Claim 1; Pages 62-63; 142pp; English.
XX
CC The present invention relates to coding sequences (see AAF44740-F44840
and AAF4843-F44844) and proteins (see AAB65714-B65814) involved in
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins
CC of the present invention are useful for modulating a PCD or cell death
CC pathway and various developmental pathways in a forestry plant, by
CC stably incorporating one of the present coding sequences into the genome
CC of the forestry plant, where the coding sequence provides a PCD pathway
CC that is not present in a native form of the forestry plant.
XX
SQ Sequence 527 BP; 98 A; 148 C; 143 G; 138 T; 0 other;
XX

Alignment Scores:
Pred. No.: 1.25e-49 Length: 527
Score: 499.50 Matches: 101
Percent Similarity: 79.72% Conservative: 13
Best Local Similarity: 70.63% Mismatches: 26
Query Match: 39.27% Indels: 4
DB: 22 Gaps: 1

US-09-955-526-4 (1-248) x AAF44783 (1-527)
QY 1 MetGluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
Db 107 ATGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 157
QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
Db 158 GATTCCCTCAAGAACTTCGCCAGATATCTCCGCCGCTCCCAATCTCACCACAGAATGTT 217
QY 41 TyrLeuThrLeuCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
Db 218 TATCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 277
QY 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 278 CTGAACATCGCGGGCTCCTCAGACAAATGCTTGCATCGAAGCATCGTGTGCTGCTGCT 337
QY 81 SerAlaProProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
Db 338 TCGATTCTCCCATGAAGAGAAAGAGGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 397

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PR	25-FEB-1999;	99US-0121825.
PR	03-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123548.
PR	23-MAR-1999;	99US-0125788.
PR	25-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130891.
PR	28-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132048.
PR	30-APR-1999;	99US-0132407.
PR	04-MAY-1999;	99US-0132484.
PR	05-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132863.
PR	11-MAY-1999;	99US-0134236.
PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	04-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.

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• •
• •

• •
• •
• •

WPI; 2003-110597/10.

Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated vascular tissue -

Claim 1; Page -; 18pp; English.

This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have antiarteriosclerotic; cytostatic; cardiatic; hypotensive; antidiabetic; gynaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-throughput methods for detecting differential expression of one or more cDNAs in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion injury, restenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new nucleic acid molecules. Antibodies to the proteins encoded by the cDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, amount or distribution of the protein. The present sequence represents a cDNA of the invention that is differentially expressed in activated vascular tissue.

Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at <http://seqdata.uspto.gov/sequence.html?docID=20020137081>.

Sequence 2994 BP: 716 A; 709 C; 682 G; 885 T; 2 other:

<hr/>					
RESULT 8					
ABX63356					
ID	ABX63356 standard; cDNA; 2994 BP.				
XX					
AC					
XX	ABX63356;				
XX					
DT	25-FEB-2003 (first entry)				
XX					
DE	Human cDNA #356 differentially expressed in activated vascular tissue.				
XX					
KW	Human; gene; ss; vascular tissue; cytostatic; atherosclerosis;				
KW	cardiant; hypotensive; antidiabetic; gynaecological; vasotropic;				
KW	cerebroprotective; gene therapy; vascular disease; cancer; coronary;				
KW	artery disease; hypertension; diabetes; pre-eclampsia; restenosis;				
KW	ischaemia-reperfusion injury; stroke;				
XX					
OS	Homo sapiens.				
XX					
PN	US2002137081-A1.				
XX					
PD	26-SEP-2002.				
XX					
PF	08-JAN-2002; 2002US-0044090.				
XX					
PR	28-JUL-2000; 2000US-222469P.				
XX					
PR	08-JAN-2001; 2001US-260483P.				
XX					
PA	(BAND/) BANDMAN O.				
XX					
PI	Bandman O;				
XX					
XX					

Alignment Scores:

Pred. NO.:	1.23e-46	Length:	2994
Score:	483.50	Matches:	102
Percent Similarity:	62.90%	Conservative:	54
Best Local Similarity:	41.13%	Mismatches:	79
Query Match:	38.01%	Indels:	13
DB:	25	Gaps:	5

US-09-955-526-4 (1-248) x ABX63356 (1-2994)

Qy	3	GlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTirpSerTyAspSer	22
Db	229	GGACCATTGCATCATTTTGAT-----CGAAGATCACTTGTATGCC	270
Qy	23	LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyLeu	42
Db	271	CTTTAAATTTTCATATAACCCGCTCAACGCAGCACCTGAAGAAGGCTCATGCA	330
Qy	43	ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrlLeuHisleLeuTrpAsn	62
Db	331	AGTTTTGCCCTTTGTATGTTTGGCGGCTGCAGGGGCTATGTCCATATGGTCACTCAT	390
Qy	63	Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetClySerMetValTrpLeuLeu	80
Db	391	TTCATTCAGGCTGGCCTGCTGCTGCCTTGGGCTCCCTGATATGTGATTTGGCTGATG	450
Qy	81	SerAlaProProTyrgln-----GluGlnLysArgValAlaLeuLeuMetAlaAla	98
Db	451	GCAACACCTCATGCCCATGAACACTGAGCAAAGAGCTGGGACTTCTGCTGGATTGCA	510
Qy	99	LeuPheGlnGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProser	118

Db 511 TTCCTTACAGGAGTTGGCCCTGGCCCTGGAGAGTTTGTATTGCTGTCAACCCGAGC 570
 QY 119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAla 138
 Db 571 ATCTTCCACGCTCTTTCATGGCGCAGCAATGATCTTTACCTGCTCACCTCAGTGCA 630
 QY 139 MetLeuAlaArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSer 158
 Db 631 CTCTATGCCAGGCGGTAGTACCTCTTTCTGGAGGTATCTGTGATGTCAGCCCTGAGC 690
 QY 159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys 178
 Db 691 TTGTTGCTT---TTGCTTCCCTGGGGAATGTTTCTTGGATCCATTGGCTTTCCAG 747
 QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198
 Db 748 GCAACCTGTATGTGGAGCTGGTGGTCAATGTCATGTGGCTTCTGTCCTTTTGATCTCACTC 807
 QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe 218
 Db 808 ATTATTGAAAGGCGCAACATGGAGATCAAGATTATATCTGGCAGCTGCATTGATCTCTTC 867
 QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu 238
 Db 868 TTAGATTTCATTACTCTCTTCAGAAACATCATGATGATCTGCGCATGAT-----GAA 921
 QY 239 LysGluGluLysLysLysLysArg 246
 Db 922 AAGGATAAAGAAGAAGAAGAA 945
 RESULT 9
 AAV59067
 ID AAV59067 standard; cDNA; 2634 BP.
 AC AAV59067;
 XX
 DT 02-FEB-1999 (first entry)
 XX
 DE Bax inhibitor BI-1 cDNA.
 XX
 KW Bax inhibitor; BI-1; human; apoptosis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 73..786
 FT /*tag= a
 XX
 PN WO9840397-A1.
 XX
 PD 17-SEP-1998.
 XX
 PF 13-MAR-1998; 98WO-0505015.
 XX
 PR 14-MAR-1997; 97US-0818514.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC, Xu Q;
 XX
 DR WPI; 1998-531519/45.
 DR P-PSDB; AAW73136.
 XX
 PT Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate
 PT cellular apoptotic activity or identify agents altering BI-1 or BI-2
 PT binding which can modulate apoptotic activity
 XX
 PS Claim 2; Page 61-63; 80pp; English.
 XX
 CC This cDNA clone codes for an inhibitor protein, termed BI-1 (see
 CC AAW73136), of the pro-apoptotic protein Bax. Nucleic acids encoding
 CC BI-1 and BI-2 (see AAV59068) were identified by suppression of
 CC Bax-induced death of yeast cells transformed to express human Bax.

CC A human HepG2 cDNA library was used for library screening. The
 CC invention provides vectors, optionally expression or viral vectors,
 CC containing BI nucleic acids, and host cells containing these
 CC vectors. The nucleic acids encoding BI-1/BI-2 can be used to
 CC increase expression of these proteins in cells, or antisense
 CC molecules prepared from them used to decrease expression. In
 CC these ways, cellular apoptotic activity may be modulated (claimed).
 CC The nucleic acids and complementary sequences are also useful as
 CC probes to detect BI-encoding nucleic acid molecules in samples.
 XX
 SQ Sequence 2634 BP; 632 A; 626 C; 597 G; 779 T; 0 other;
 Alignment Scores:
 Pred. No.: 3,05e-46 Length: 2634
 Score: 479.50 Matches: 101
 Percent Similarity: 62.90% Conservative: 55
 Best Local Similarity: 40.73% Mismatches: 79
 Query Match: 37.70% Indels: 13
 DB: 19 Gaps: 5
 US-09-955-526-4 (1-248) x AAV59067 (1-2634)
 QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTyrSerTyrAspSer 22
 Db 67 GGNACCATGACATATTTCAT-----CGAAGATCACTTTGATGCG 108
 QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42
 Db 109 CTTTAAATTTTCTCATATACCCGCTCAACCCAGCAGCAGCCTGAAGAGTCTATGCA 168
 QY 43 ThrLeuLysCysAlaLeuValAlaSerAlaGlyAlaTyrLeuHisIleLeuTyrAsn 62
 Db 169 AGTTTTCGCTTGTATGTTTGGCGCTGCAGGGCCCTATGTCATATGTCATCATCAT 228
 QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTyrLeu 80
 Db 229 TTCATTACGCTGGCCCTGCTGCTGCTGGGCTCCCTGATATGATGATTTGGCTGATG 288
 QY 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAla 98
 Db 289 GCAACACCTCATAGCCATGAAACTGAACAGAAATACTGGGACTCTTCTGCTGATTTGCA 348
 QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118
 Db 349 TTCCTTACAGGAATTTGGCTGGCCCTGCTGCTGGAGTTTGTATGCTGTACACCCAGC 408
 QY 119 IleValPheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaAla 138
 Db 409 ATCCTTCCCACTGCTTTTCATGGCGCAGGCAATGATCTTTACCTGCTTCACTCAGTGCA 468
 QY 139 MetLeuAlaArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSer 158
 Db 469 CTCTATGCCAGGCGCGGTAGTACCTCTTCTGGAGGTATCTTGTATGTCAGCCCTGAGC 528
 QY 159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys 178
 Db 529 TTGTTGCTT---TTGCTTCCCTGGGGAATGTTTCTTGGATCCATTGGCTTTCCAG 585
 QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198
 Db 586 GCAACCTGTATGTGGAGCTGGTGGTCAATGTCATGTTGCTTCTGCTTGTATCACTCACTC 645
 QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe 218
 Db 646 ATTATTGAAAGGCGCAACATGGAGATCAAGATTATATCTGGCAGCTGCATTGATCTCTTC 705
 QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu 238
 Db 706 TTAGATTTCATTACTCTCTTCAGAAACATCATGATGATCTGCGCATGAT-----GAA 759
 QY 239 LysGluGluLysLysLysLysArg 246
 Db 760 AAGGATAAAGAAGAAGAAGAA 783

RESULT 10

ABK84658
ID ABK84658 standard; cDNA; 2600 BP.
XX AC
XX ABK84658;
XX
XX 14-AUG-2002 (first entry)
XX
XX Human cDNA differentially expressed in granulocytic cells #1229.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
XX Homo sapiens.
XX
XX WO200228999-A2.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US30821.
XX
XX 03-OCT-2000; 2000US-237189P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX WPI; 2002-435328/46.
XX
XX Detecting granulocyte activation by detecting differential expression
XX of genes associated with granulocyte activation, which serves as
XX diagnostic markers that is useful for monitoring disease states and
XX drug toxicity -
XX
XX Claim 1; SEQ ID NO 1229; 114pp; English.
XX
XX The invention relates to detecting (M1) granulocyte (GC) activation
XX (GCA), by detecting the level of expression of gene(s) (Gs) identified by
XX DNA chip analysis as given in the specification, and comparing
XX the expression level to an expression level in an unactivated
XX GC, where differential expression of Gs is indicative of GCA.
XX Also included are modulating (M2) GA by contacting GC with an agent
XX that alters the expression of at least one gene in Gs; (2) screening (M3)
XX for an agent capable of modulating GCA or an inflammation (especially
XX chronic) in a tissue, an allergic response in a subject, exposure of a
XX subject to a pathogen or sterile inflammatory disease using the
XX gene expression profile; (3) detecting (M4) an inflammation (especially
XX chronic) in a tissue, an allergic response in a subject, exposure of a
XX subject to a pathogen or sterile inflammatory disease, by detecting the
XX level of expression in a sample of the tissue of gene(s) from Gs, where
XX the level of expression of the gene is indicative of inflammation;
XX (4) treating (M5) an inflammation (especially chronic) or in a tissue,
XX or allergic response in a subject, exposure of a subject to a pathogen
XX or sterile inflammatory disease, by contacting a tissue having
XX inflammation with an agent that modulates the expression of gene(s)
XX from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
XX modulating GA; M3 is useful for screening an agent capable of modulating
XX GCA preferably in an inflammation in a tissue; M4 is useful for
XX detecting an inflammation (especially chronic) in a tissue, an allergic
XX response in a subject, exposure of a subject to a pathogen or sterile
XX inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
XX glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
XX reperfusion injury, ARDS, adult respiratory distress syndrome,
XX inflammatory bowel disease, Crohn's disease, ulcerative colitis,
XX periodontal disease; also bacterial infection, viral infection,
XX parasitic infection, protozoal infection, fungal infection and M5 is

CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 2600 BP; 619 A; 621 C; 590 G; 770 T; 0 other;

Alignment Scores:

Pred. No.:	1.54e-45	Length:	2600
Score:	473.50	Matches:	101
Percent Similarity:	62.10%	Conservative:	53
Best Local Similarity:	40.73%	Mismatches:	81
Query Match:	37.22%	Indels:	13
DB:	24	Gaps:	5
US-09-955-526-4 (1-248) x ABK84658 (1-2600)			
QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22			
Db 35 GGAACCATGAACATATTTGAT-----CGAAGATCAACTTTGATGCG 76			
QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42			
Db 77 CTTTAAATTTTCTCATATAACCCCGTCAACGACGACGACACCTGAAGAAGGTCTATGCA 136			
QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsn 62			
Db 137 AGTTTGGCCCTTTGATGTTTGTGGCGCTGCGAGGCGCTATGTCATATGGTCACTCAT 196			
QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80			
Db 197 TTCATTGAGGCTGGCGCTGCTGCGCTGGGCTCCCTGATATGATGATTTGGCTGATG 256			
QY 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAlaAla 98			
Db 257 GCAACACCTCATAGCCATGAACCTGAACAGAAAGACTGGGACTTCTTGTGGATTGCA 316			
QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118			
Db 317 TTCCTTACAGGAGTTGGCGCTGGCGCTGGAGTTTGTATTGTCTCAACCCCGAGC 376			
QY 119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAla 138			
Db 377 ATCCTTCCCCTGCTTCATGCGGCACAGCAATGATCTTTACCTGCTTCACTCAGTGCA 436			
QY 139 MetLeuAlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSer 158			
Db 437 CTCATATGCCAGGCGCGCTAGCTACCTCTTTCTGGAGGATATCTGTATGTGAGCCCTGAGC 496			
QY 159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys 178			
Db 497 TTGTGCTT---TTGCTTCCCTGGGAAATGTTTCTTTGGATCCCAITTTGGCTTCCAG 553			
QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198			
Db 554 GCAACACCTGATGTGGGACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613			
QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValIlyHisAlaLeuThrLeuPhe 218			
Db 614 ATTATTGAAAGCCGCAACATGGAGATCAAGATTATATCTGGCATTCGATTCCTCTTC 673			
QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleIleMetLeuLysAsnAlaSerGlu 238			
Db 674 TTGATTTCAATTACTGCTTCACAAAACCTCATGATGATGCTGCTGCTGCTGCTGCTGCT 727			
QY 239 LysGluGluLysLysLysLysArg 246			
Db 728 AAGGATAAGAAAGAAAGAAAGAA 751			

RESULT 11
ABX19768

of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 751 BP; 163 A; 177 C; 185 G; 225 T; 1 other;

Alignment Scores:

Pred. No.: 1,55e-35 Length: 751
Score: 382.50 Matches: 87
Percent Similarity: 59.36% Conservative: 43
Best Local Similarity: 39.73% Mismatches: 78
Query Match: 30.07% Indels: 12
DB: 24 Gaps: 4

US-09-955-526-4 (1-248) x ABQ56073 (1-751)

QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyAspSer 22
Db 60 GGAACCATGAACATATTGAT-----CGAAGATCAACITTGATCGG 101
QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyLeu 42
Db 102 CTTTAAATTTCTCATATAACCCGTCACGAGCAGCAGCCCTGAAGAAGGCTATGCA 161
QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyLeuHisIleLeuTrpAsn 62
Db 162 AGTTTGGCCCTTGATGTTGTGGCGCTGCAGGGCCCTATGTCATATGGFCACTCAT 221
QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 222 TTCATTACGGCTGGCGTGTGCTGCTGGGCTCCCTGATATGATGTTGGCTGATG 281
QY 81 SerAlaProProTyrgln-----GluGlnLysArgValAlaLeuLeuMetAlaAla 98
Db 282 GCAACACCTCFATAGCCATGAAACTGAACAGAAAGACTGGGACTTCTGCTGGATTGCA 341
QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118
Db 342 TTCTTTACAGGAGTTGGCTGGCCCTGCCCTGGAGTTTGTATTGCTGTCAACCCAGC 401
QY 119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAla 138
Db 402 ATCTTCCCACTGCTTTCATGGCAGCGCAATGATCTTTACCTGCTTCACTCCCTCAGTGCA 461
QY 139 MetLeuAlaArgArgGluTyLeuTyLeuTyLeuGlyGlyLeuSerSerGlyValSer 158
Db 462 CTCATGCGCAGGCGCGTAGTACCTCTTCTGGGAGGTATCTGTATGTCACGCCCTGAG 521
QY 159 LeuLeuPheTrpLeuHisPheAlaSerIlePheGlyGlySerMetAlaValPheLys 178
Db 522 CTGGTGGCTTTGCTTCCCTGGGAAAGGTTTCCTTT---GGATCCATTGGCTTTCCAG 578

QY 179 PheGluLeuTyrrPheGlyLeuLeuValPheValGlyTyrrIleValPheAspThrGlnGlu 198
Db 579 GCAAACTGTATWGGAGCTGGTGCACTGTGGCTTCGC-CTTTTGATACTCACTC 637
QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrrValLysHisAlaLeuThrLeu 217
Db 638 ATTATTGAAAGGCCGCAACATGGAGATCAAGATTATATCTGGCACATGATGATCTC 694

RESULT 13

ABV88094/C

ID ABV88094 standard; cDNA; 536 BP.

XX AC ABV88094;

XX DT 13-DEC-2002 (first entry)

XX DE Human colon cancer related cDNA SEQ ID NO 1405.

XX KW Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine; gene; ss.

XX OS Homo sapiens.

XX PN WO200258534-A2.

XX PD 01-AUG-2002.

XX PF 19-NOV-2001; 2001WO-US43704.

XX PR 20-NOV-2000; 2000US-252222P.

XX PR 06-FEB-2001; 2001US-267011P.

XX PR 28-MAR-2001; 2001US-279670P.

XX PR 10-JUL-2001; 2001US-304037P.

XX PA (CORI-) CORIXA CORP.

XX PI Sulk JA, Xu J, Chenault RA, Meagher MJ, Secret H, King GE;

XX DR WPI; 2002-608400/65.

XX PT New isolated tumor colon polynucleotide and polypeptide, useful for the diagnosis, prevention and/or treatment of cancer, in particular colon cancer -

XX PS Claim 1; SEQ ID NO 1405; 266pp + Sequence Listing; English.

XX CC The invention relates to a human colon tumour expressed polynucleotide (i) encoding a polypeptide (ii, ABP67991-ABP67996) comprising: (i) any of 2500 fully defined nucleotide sequences (ABV8669-ABV89289); (ii) complements of (i); (iii) at least 20 contiguous residues of (i); (iv) sequences that hybridize to (i), under moderately stringent conditions; (v) sequences having at least 75% or 90% identity to (i); or (vi) degenerate variants of (i). The compositions and methods of the present invention are useful for the diagnosis, prevention and/or treatment of cancer, particularly colon cancer. (i) can be used in gene therapy and (i) and (ii) are useful in pharmaceutical compositions such as vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 536 BP; 176 A; 122 C; 133 G; 105 T; 0 other;

Alignment Scores:

Pred. No.: 1,91e-34 Length: 536
Score: 371.50 Matches: 76
Percent Similarity: 65.88% Conservative: 36
Best Local Similarity: 44.71% Mismatches: 55
Query Match: 29.21% Indels: 3
DB: 24 Gaps: 2

US-09-955-526-4 (1-248) x ABV88094 (1-536)

QY 65 GlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProPro 84

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Db 508 GGCGCTGCTGCTGCCCTGGGCTCCCTGATATGATGATTGGCTGATGCAACACCTCAT 449
Qy 85 TyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPheGluGly 102
Db 448 AGCCATGAACACTGAACAGAAAGACTGGGACTTCTTGGTGGAFTTGCATTCCTTACAGGA 389
Qy 103 AlaserileGlyProLeuLeuGluLeuGlyLeuAsnPheAspProSerileValPheGly 122
Db 388 GTTGGCTGGCCCTGCCCTGGAGTTTGTATTGCTGTCAACCCAGCATCTTCCCACT 329
Qy 123 AlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeuAlaArg 142
Db 328 GCTTTATGGGCGCGGCAATGATCTTTACCTGCTTCCCTCAGTGCACCTCTATGCCAGG 269
Qy 143 ArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeuPheTip 162
Db 268 CGCGGTAGCTACCTCTTCTGGAGGTATCTTGATGTCACCCCTGAGCTTGTGTCTT--- 212
Qy 163 LeuHisPheAlaSerSerilePheGlyGlySerMetAlaValPheLysPheGluLeuTyr 182
Db 211 TTGTCTTCCCTGGGAATGTTTCTTTGGATCCATTGGCTTTTCCAGGCAAACTGTAT 152
Qy 183 PheGlyLeuLeuValPheValGlyTyrileValPheAspThrGlnGluLeuLys 202
Db 151 GTGGGACTGTGTGTCATGTGTGGCTTGTGCTCTTTTGTATCTCAACTCATATTGAAAG 92
Qy 203 AlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGly 222
Db 91 GCCGAACATGGAGATCAAGATTATATCTGCGACTGCATTGATCTCTTCTTAGATTTCATT 32
Qy 223 AlaValPheValArgLeuLeuLeuMet 232
Db 31 ACTGTCTTCCAGAAACTCATGATGATCCTG 2
```

RESULT 14

ABLI12505
ID ABLI12505 standard; cDNA; 1085 BP.

XX AC ABLI12505;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31997.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.

XX FN WO2001/1042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.

XX PR 23-MAR-2000; 2000US-191637P.

XX PR 11-JUL-2000; 2000US-0614150.

XX PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX DR P-PSDB; ABB68402.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

XX PS Claim 1; SEQ ID NO 31997; 21pp + sequence listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI16176-ABL30511), expressed DNA sequences (ABLI01840-ABLI16175) and the encoded proteins (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1085 BP; 299 A; 263 C; 239 G; 284 T; 0 other;

Alignment Scores:

Pred. No.:	6,04e-27	Length:	1085
Score:	312.00	Matches:	77
Percent Similarity:	55.80%	Conservative:	48
Best Local Similarity:	34.38%	Mismatches:	83
Query Match:	24.53%	Indels:	16
DB:	23	Gaps:	5

US-09-955-526-4 (1-248) x ABLI12505 (1-1085)

```
Qy 31 ProLeuValGlnThrHisLeuLysGlnValTyrLeuThrLeuCysCysAlaLeuValAla 50
Db 231 CCTATGTGGCGAGCACCTGTCTAGGTTTACATGCTCTGGCAGCAGCTGCGCTGCC 290
Qy 51 SerAlaGlyAlaTyrLeuHisIle-----LeuTrpAsnIleGlyLeuLeuThr 68
Db 291 ACGGCCATGGAGCCATGCTTCAGATCGGAGCTTTCTCGATCTTGA----- 338
Qy 69 ThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProTyrGlnGluGln 88
Db 339 GTCTGGCGCGGTGGCCACTAGTCTGCTGTGGCTGTGCACTTCTCAAGAGGATGAC 396
Qy 89 -----LysArgValAlaLeuMetAlaAlaLeuPheGluGlyAla 103
Db 399 GGCNAGAACTATTATACACGTTGGGATGCTCTACGCTTCGGATCTCTCCGGCAG 458
Qy 104 SerileGlyProLeuLeuGluLeuGlyIleAsnPheAspProSerileValPheGlyAla 123
Db 459 ACGCTCGACCGCTCTCGCTATATATGACGACATAAATCCGGCAATAATCTGTCTGCC 518
Qy 124 PheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeuAlaArg 143
Db 519 CTTACGGGCGACCTTCGTCACCTTCATCTGCTCTCTGTCGCGCTTCTGGCGAGCAG 578
Qy 144 ArgGluTyrLeuTyrLeuGlyLeuSerSerGlyValSerLeuLeuPheTrpLeu 163
Db 579 GGCAAGTACCTCTATCTGGTGGGATGCTGTGTAGCGTCATCAACACCATGGCGCTCTG 638
Qy 164 HisPheAlaSerSerilePheGlyGlySerMetAlaValPheLysPheGluLeuTyrPhe 183
Db 639 AGTCTCTTAACATGGTCTTC---AAGTCCTACTTCTGCAAGTGAAGTCACTTACGTC 695
Qy 184 GlyLeuLeuValPheValGlyTyrileValPheAspThrGlnGluLeuLysAla 203
Db 696 GCGTTTTTCGTTATGGTGGCTTCATGCTTACCATACAGAACATTTGGAGAAAGTC 755
Qy 204 HisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAla 223
Db 756 CGAAACGGAAATCGAGATGTGTCAGCACGCTTTAGATTGTCTTCGATGTACTCAGC 815
Qy 224 ValPheValArgIleLeuIleMetLeuLysAsnAlaSerGluLysGluLysLys 243
Db 816 ATGTTCCGCCCTTGGCTGATTATATCTG-----ACGCAAAAGGAGGAGCGAA 863
Qy 244 LysLysArgArg 247
Db 864 CAGAAATGAACGC 875
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RESULT 15
ABV25317

ID ABV25317 standard; cDNA; 638 BP.
 XX AC ABV25317;
 XX DT 16-SEP-2002 (first entry)
 XX XX Human prostate expression marker cDNA 25308.
 XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW KW pharmacogenomic marker; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200160860-A2.
 XX PD 23-AUG-2001.
 XX PF 20-FEB-2001; 2001WO-US05171.
 XX PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 PI WPI; 2001-662795/76.
 DR Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX Claim 1; Page 4984; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 638 BP; 129 A; 155 C; 163 G; 191 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 4.2e-27 Length: 638
 Score: 310.50 Matches: 68
 Percent Similarity: 56.50% Conservative: 45
 Best Local Similarity: 34.00% Mismatches: 62
 Query Match: 24.41% Indels: 25
 DB: 23 Gaps: 4
 US-09-955-526-4 (1-248) x ABV25317 (1-638)
 QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22
 Db 89 GGAACCATGACATATTTGAT-----CGAAGATCAACTTTGATGCG 130
 QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42
 Db 131 CTTTAAATTTCTCATATAACCCGTCACGACGACCACTGAAGAGGCTATGCA 190

Search completed: September 22, 2003, 15:34:05
 Job time : 273 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	688.5	54.1	884	4	US-09-325-932A-43	Sequence 4
2	499.5	39.3	527	4	US-09-325-932A-44	Sequence 4
3	479.5	37.7	2634	2	US-08-818-514-1	Sequence 1
C	479.5	37.7	2634	2	US-08-818-514-2	Sequence 2
5	479.5	37.7	2634	3	US-09-115-934A-1	Sequence 1
C	479.5	37.7	2634	3	US-09-115-934A-2	Sequence 2
6	479.5	37.7	2634	4	US-09-611-175-1	Sequence 1
7	479.5	37.7	2634	4	US-09-611-175-2	Sequence 1
C	479.5	37.7	2634	4	US-09-611-175-2	Sequence 2
9	188	14.8	601	3	US-09-385-982-231	Sequence 2
10	165	13.0	1316	4	US-09-362-123A-1	Sequence 1
11	165	13.0	1596	4	US-09-149-476-184	Sequence 1
12	165	13.0	1943	4	US-09-996-243-1	Sequence 1

Result No.	Score	Query Match	Length	DB	ID	Description
1	688.5	54.1	884	4	US-09-325-932A-43	Sequence 4
2	499.5	39.3	527	4	US-09-325-932A-44	Sequence 4
3	479.5	37.7	2634	2	US-08-818-514-1	Sequence 1
C	479.5	37.7	2634	2	US-08-818-514-2	Sequence 2
5	479.5	37.7	2634	3	US-09-115-934A-1	Sequence 1
C	479.5	37.7	2634	3	US-09-115-934A-2	Sequence 2
7	479.5	37.7	2634	4	US-09-611-175-1	Sequence 1
C	479.5	37.7	2634	4	US-09-611-175-2	Sequence 2
9	188	14.8	601	3	US-09-385-982-231	Sequence 2
10	165	13.0	1316	4	US-09-362-123A-1	Sequence 1
11	165	13.0	1596	4	US-09-149-476-184	Sequence 1
12	165	13.0	1943	4	US-09-996-243-1	Sequence 1


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DB:                2                5
US-09-955-526-4 (1-248) x US-08-818-514-1 (1-2634)

QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22
Db 67 GGAACCATGAACATATTGAT-----CGAAAGATCAACTTTGATGG 108

QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42
Db 109 CTTTAAATTTCTCATATACCCGTCACGAGCCGCTATGCTCATATGCTCACTCAT 168

QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTyrAsn 62
Db 169 AGTTTGGCCCTTGTATGTTGTTGGGGCTGACGGGGCTATGCTCATATGCTCACTCAT 228

QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 229 TTCATTACAGGCTGGCGTCTGCTGCTGGCTGGCTGCTCATATGATGATTTGGCTGATG 288

QY 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAla 98
Db 289 GCAACACCTCATAGCCATGAACCTGAACAGAAAAAAGCTGGGACTTCTTCTGGATTTGCA 348

QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118
Db 349 TTCTTACAGGAATTTGGCTGGCCCTGCTGGAGTTTGTATGCTGTCAACCCAGC 408

QY 119 IleValPheGlyAlaPheValGlyCysAlaValAlaPheGlyCysPheSerAlaAla 138
Db 409 ATCTTCCCACTGCTTTCATGGGACGGAATGATCTTTACCTGCTTCAACCTCAGTGCA 468

QY 139 MetLeuAlaArgArgGlnTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSer 158
Db 469 CTTATGCGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528

QY 159 LeuLeuPheTrpLeuHisPheAlaSerIlePheGlyGlySerMetAlaValPheLys 178
Db 529 TTGTTGCTT---TTGCTTCCCTGGGGAATGTTTCTTTGGATTCATTTGGCTTTCCAG 585

QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198
Db 586 GCAACACCTCATGTTGGAGCTGTTGGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645

QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe 218
Db 646 ATTATGAAAGCCGCAACATGGAGATCAAGATATATATCTGGCAGCTGCAITGATCTCTC 705

QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu 238
Db 706 TTAGATTTCATTACTCTCTCAGAAAACTCATGATGATCTGSCCATGAAT-----GAA 759

QY 239 LysGluGluLysLysLysArg 246
Db 760 AAGGATAGAGAGAGAGAGAGAA 783

RESULT 4
US-08-818-514-2/c
; Sequence 2, Application US/08818514
; Patent No. 5837838
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,514
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-818-514-2

Alignment Scores:
Pred. No.:      8,9e-53      Length:      2634
Score:          479.50      Matches:     101
Percent Similarity: 62.90%    Conservative: 55
Best Local Similarity: 40.73% Mismatches:    79
Query Match:      37.70%     Indels:     13
DB:               2         Gaps:         5

US-09-955-526-4 (1-248) x US-08-818-514-2 (1-2634)

QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22
Db 2568 GGAACCATGAACATATTGAT-----CGAAAGATCAACTTTGATGG 2527

QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42
Db 2526 CTTTAAATTTCTCATATACCCGCTCAACGACGACGCTGAGAGGCTCATGCA 2467

QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTyrAsn 62
Db 2465 AGTTTGGCCCTTGTATGTTGTTGGCGCTGACGGGGCTATGCTCATATGGTCACTCAT 2407

QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 2406 TTCATTACAGGCTGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2347

QY 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAla 98
Db 2346 GCAACACCTCATAGCCATGAACCTGAACAGAAAAAAGCTGGGACTTCTTCTGGATTTGCA 2287

QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118
Db 2286 TTCCTTACAGGAATTTGGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2227

QY 119 IleValPheGlyAlaPheValGlyCysAlaValAlaPheGlyCysPheSerAlaAla 138
Db 2226 ATCTTCCCACTGCTTTCATGGGACGGAATGCTTTACCTGCTTCAACCTCAGTGCA 2167

QY 139 MetLeuAlaArgArgGlnTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSer 158
Db 2166 CTTATGCGAGCGCGCTAGCTACCTTTCTTGGGAGGATCTTGTATGTCAGCCCTGAGC 2107

QY 159 LeuLeuPheTrpLeuHisPheAlaSerIlePheGlyGlySerMetAlaValPheLys 178
Db 2106 TTGTTGCTT---TTGCTTCCCTGGGGAATGTTTCTTGGATTCATTTGGCTTTTCCAG 2050

QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198
Db 2049 GCAACACCTGATGTTGGGACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1990

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43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyValaTyrlLeuHisIleLeuTriPAsn 62
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
169 AGTTTGGCCCTTGTATGTTTGGCGGCTGCAGGGCCCTATGTCATATGCTACTCAT 228
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
229 TTCATTCCAGGCTGGCCGCTGCTGCTTGGGCTCCCTGATATGATGATTTGGCTGATG 288
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
63 Ile-----GlyGlyLeuLeuThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
229 TTCATTCCAGGCTGGCCGCTGCTGCTTGGGCTCCCTGATATGATGATTTGGCTGATG 288
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
81 SerAlaProProTyrGln-----GluGlnLysArgValAlaIleuLeuMetAlaAla 98
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
289 GCAACACCTCATAGCCCATGAAACTGAACAGAAAAAAGCTGGGACTCTCTCTCGTGGATTGCA 348
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
99 LeuPheGluGlyAlaSerIleGlyProLeuIleLeuGlyIleLeuPheAspProSer 118
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
349 TTCCTTACAGAAATGGCTGGGCCCTGGCCCTGGAGTTTGTATTGCTGTCAACCCAGC 408
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAla 138
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
409 ATCTCTCCCATGCTTCATCGGCACGGCAATGATCTTACCTGCTTCACCTCAGTGCA 468
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
139 MetLeuAlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSer 158
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
469 CTCATGCGCAGCGCCGTAGCTACCTCTTCTGGAGGATATCTTGATGTCAGCCCTGAGC 528
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyCysSerMetAlaValPheLys 178
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
529 TTGTTGCTT---TGTCTCTCCCTGGGGAATGTTTCTTTGGATCCATTTGGCTTTTCCAG 585
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
586 GCAACACCTGTATGCGGACTGGTGGTCATGTGTGGCTTCGTCTCTTTGATCTCACTCACT 645
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe 218
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
646 ATATTGAAAGGCCCAACATGAGATCAAGATATATATCTGGCACTGCATTTGATCTCTTC 705
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
219 ThrAspPheGlyAlaValPheValArgIleLeuIleLeuMetLeuLysAsnAlaSerGlu 238
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
706 TTAGATTTCATTACTGCTCTTCAGAAAAGCTCATGATGATCTCGCCCATGAAT-----GAA 759
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
239 LysGluGluLysLysLysLysArg 246
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
760 AAGGATAGAGAAAGAGAGAGAAA 783
   |||||::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

RESULT 6
US-09-115-934A-2/c
; Sequence 2, Application US/09115934A
; Patent No. 6130317
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115.934A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/818,514
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:

```



```

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-115-934A-2

Alignment Scores:
Pred. No.: 8.9e-53 Length: 2634
Score: 479.50 Matches: 101
Percent Similarity: 62.90% Conservativeness: 55
Best Local Similarity: 40.73% Mismatches: 79
Query Match: 37.70% Indels: 13
DB: 5 Gaps: 5

US-09-955-526-4 (1-248) x US-09-115-934A-2 (1-2634)
QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22
Db 2568 GSAACCATGACATATTTGAT-----CGAAGATCAACTTTGATGCG 2527
QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42
Db 2526 CTTTAAATTTCTCATATACCCGTCACGCAGCAGCCCTGAAGAAGGCTATGCA 2467
QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsn 62
Db 2466 AGTTTGGCCTTTGTATGTTGTGGCGGCTGACGGGCTATGCTCCATATGGTCACTCAT 2407
QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 2406 TTCATTGAGCTGGCTGCTGCTGCTGGGCTGCCCTGATATGATGATTTGGCTGATG 2347
QY 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAla 98
Db 2346 GCACACCTCATAGCATCAACTGACACGACGACGACGACGACGACGACGACGACGACGAC 2287
QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118
Db 2286 TTCCTTACAGGAATGGCCTGGGCGCTGCGCTGGAGTTTGTATGCTGTCAACCCGAGC 2227
QY 119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAla 138
Db 2226 ATCCTTCCGACTGCTTTCATGAGGACGACGACGACGACGACGACGACGACGACGACGAC 2167
QY 139 MetLeuAlaArgArgGlyTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSer 158
Db 2166 CTCATGACGAGGCGGCTAGTACCTCTTCTGGAGGATCTGTATGTCAGCCCTGAGC 2107
QY 159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys 178
Db 2106 TTGTTGCTT---TTGCTTCCCTGGGGAATGTTTCTTGGATCCCACTTTGGCTTTCCAG 2050
QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198
Db 2049 GCAACCTGATGTGGAGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1990
QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe 218
Db 1989 ATTATTGAAAGCCGCAACATGAGATCAAGATTATATCTGGCACTCCATGATCTCTTC 1930
QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu 238
Db 1929 TTAGATTCTATTACTGCTTTCAGAAACCTCATGATGCTGCTGCTGCTGCTGCTGCTGCT 1876
QY 239 LysGluLeuLysLysLysArg 246

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Db 1875 AAGGATAAGAAAGAAAGAGAGAA 1852
RESULT 7
US-09-611-175-1
; Sequence 1, Application US/09611175
; Patent No. 6545128
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,175
; FILING DATE: 06-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,934
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/818,514
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-611-175-1

Alignment Scores:
Pred. No.: 8.9e-53 Length: 2634
Score: 479.50 Matches: 101
Percent Similarity: 62.90% Conservativeness: 55
Best Local Similarity: 40.73% Mismatches: 79
Query Match: 37.70% Indels: 13
DB: 5 Gaps: 5

US-09-955-526-4 (1-248) x US-09-611-175-1 (1-2634)
QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22
Db 67 GGAACCATGACATATTTGAT-----CGAAGATCAACTTTGATGCG 108
QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42
Db 109 CTTTAAATTTCTCATATACCCGTCACGCAGCAGCCCTGAAGAAGGCTATGCA 168
QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsn 62
Db 169 AGTTTGGCCTTTGTATGTTGTGGCGGCTGACGGGCTATGCTCCATATGGTCACTCAT 228
QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80

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RESULT 9
US-09-385-982-231
; Sequence 231, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: 11
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(601)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-231

Alignment Scores:
Pred. No.: 2,27e-15 Length: 601
Score: 188.00 Matches: 56
Percent Similarity: 51.98% Conservative: 36
Best Local Similarity: 31.64% Mismatches: 65
Query Match: 14.78% Indels: 22
DB: Gaps: 6

US-09-955-526-4 (1-248) x US-09-385-982-231 (1-601)

Qy 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22
   |||   ::|   |||||   ::|   ::|   ::|   ::|   ::|   ::|   ::|   ::|
Db 91 GGAACCATGAACATATTGAT-----CGAAAGATCAACTTGTATGGG 132

Qy 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42
   |||   |||   |||||   |||   |||||   |||   |||||   |||   |||||   |||
Db 133 CTTTAAAAATTTCTCATATAACCCCGTCAACGCAGCAGCACCTGAAGAAGTCTATGCA 192

Qy 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsn 62
   ::|   ::|   ::|   ::|   ::|   ::|   ::|   ::|   ::|   ::|   ::|
Db 193 AGTTTGGCCCTTGATGTTGTGGCGGCTGACGGGCTTAIGTCATATGTCACATCAT 252

Qy 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
   |||||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db 253 TTCATTACGGCTGGGCTGCTGCTGCTGCTGGGCTCCCTCATATTGATGATTGGCTGATG 312

Qy 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAlaAla 98
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Qy 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118
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Qy 159 LeuLeuPhe-----TrpLeuHisPheAlaSerSer 168
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

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1 / APPLICANT: Roy, Margaret Ann
2 / APPLICANT: Stewart, Timothy A.
3 / APPLICANT: Tumas, Daniel
4 / APPLICANT: Watanabe, Colin K.
5 / APPLICANT: Williams, P. Mickey
6 / APPLICANT: Wood, William I.
7 / APPLICANT: Zhang, Zemin
8 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
9 / TITLE OF INVENTION: Acids Encoding the Same
10 / FILE REFERENCE: P2730PIC13
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US-09-955-526-4 (1-248) x US-09-996-243-1 (1-1943)

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; NAME/KEY: misc_feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1349491)..(1349491)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
; US-08-916-421B-1

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Alignment Scores:

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Pred. No.: 0.544
Score: 120.50
Percent Similarity: 36.86%
Best Local Similarity: 23.14%
Query Match: 9.47%
Length: 1664976
Matches: 59
Conservative: 35
Mismatch: 73
Indels: 89

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DB: 4 Gaps: 12
US-09-955-526-4 (1-248) x US-08-916-421B-1 (1-1664976)
QY 45 CysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsnIleGly 64
DB 1638230 TGTGTTTATTGGTT-----CATTTGAAATGGAAT----- 1638201
QY 65 GlyLeuLeu-----ThrThrMetAlaCysMetGlySer 75
DB 1638200 GGACATTTATGAAGAGATATTGGATGTATATAAATAAAGCTCGATATCTGGCTTTA-TTA 1638142
QY 76 MetValTrpLeuSerAlaProProTyrGlnGlnLysArgValAlaLeuLeuMet 95
DB 1638141 ATTGTTGGATTATATCGGAATAGTATTAACTTTGCTTTCATCTTCCAATCTTATCA 1638082
QY 96 AlaAlaLeuPheGluGlyAlaSerIleGly-----Pro 107
DB 1638081 TTGATTGGATTGCTATTATTGGGGCTATCGTTTGGGCTACTGACCCCTGCTACATTAAATACCA 1638022
QY 108 LeuIle-----GluLeuGlyIleAsnPheAspProSerIleVal 120
DB 1638021 ATATTCTCAAGCATGATATTGANCACAGATAGCAATAACCTTAGAACACAGAGTGT 1637962
QY 121 PheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaMetLeu 140
DB 1637961 TTTAACGACCCATTAGGATTGTTGTAACACTTATATGTTATACGCCCTTGGTTTAGCT 1637902
QY 141 AlaArgArgArg-----GluTyr-----LeuTyrLeuGlyGlyLeuLeu----- 153
DB 1637901 AAAGCTGAGAAATCCAAATCTTGAAATTTTTCATTAGCTGTGGTGGGATAATATTGGGG 1637842
QY 153 ----- 153
DB 1637841 GTTATAGCAGGCAAGTTCTATGAATTTATATCTCAAAAATTAAGTTTGAGGACTATATT 1637782
QY 154 -----SerSerGlyValSerLeuLeuPheTrpLeuHisPheAlaSerSerIlePhe 170
DB 1637781 GCTCCATTACTTTAGGATGGCTATTGCCCTTTGG--TATTTGCTGAGGGAATTTTC 1637725
QY 171 -----GlyGlySerMetAlaValPheLysPheGluLeuTyr 182
DB 1637724 CCATCAATAAATCGCTATGAATTTAGTGGATTATGGCAGTGGCTATAATGGGATTATAT 1637665
QY 183 PheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleIleGluLys 202
DB 1637664 ATTGGAACGTCATA-----GTGCATAAAAAA 1637638
QY 203 AlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGly 222
DB 1637637 GAACATAAAAAAGATATGAAAAGGTT-----GCAGTGTATTATGATGCAACTC 1637590
QY 223 AlaValPheValArgIleIleIleMetLeuLysAsnAlaSer 237
DB 1637589 TCCATATTATCAGATAATTAATCTCGTATTATTAGGGGCAAGT 1637545
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Search completed: September 22, 2003, 17:01:35
Job time : 341 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: September 22, 2003, 16:21:19 ; Search time 246 Seconds
(without alignments)
2479.917 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MGFSTFFDSQASRNRWSY.....LIIMLKNASEKKEKKKKRRN 248

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Db=Published Applications_NA -QWMT=Fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0955526.cgn1.1.333 -runat_22092003.151757.12511
-NCPU=6 -ICPU=3 -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Published Applications_NA:

1: /cgn2.6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2.6/ptodata/2/pubpna/PT_NEW_PUB.seq:
3: /cgn2.6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2.6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2.6/ptodata/2/pubpna/US07_NEW_PUB.seq:
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7: /cgn2.6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2.6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2.6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2.6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2.6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2.6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2.6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2.6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2.6/ptodata/2/pubpna/US10_NEW_PUB.seq:
16: /cgn2.6/ptodata/2/pubpna/US60_NEW_PUB.seq:
17: /cgn2.6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1272	100.0	1034	11	US-09-955-526-3

2	1027.5	80.8	1009	9	US-09-770-445-223	Sequence 223, Appl
3	988	77.7	735	14	US-10-167-015-15	Sequence 15, Appl
4	963.5	75.7	1218	14	US-10-219-220-232	Sequence 232, Appl
5	955	75.1	989	14	US-10-167-015-17	Sequence 17, Appl
6	884.5	69.5	1026	14	US-10-167-015-31	Sequence 31, Appl
7	879	69.1	1138	14	US-10-167-015-33	Sequence 33, Appl
8	879	69.1	1139	14	US-10-167-015-5	Sequence 5, Appl
9	871	68.5	1026	14	US-10-167-015-3	Sequence 3, Appl
10	786.5	61.8	957	14	US-10-167-015-1	Sequence 1, Appl
11	772.5	60.7	1102	14	US-10-219-220-231	Sequence 231, Appl
12	688.5	54.1	884	14	US-10-219-220-43	Sequence 43, Appl
13	499.5	39.3	527	14	US-10-219-220-44	Sequence 44, Appl
14	491.5	38.6	873	12	US-10-263-828-6	Sequence 6, Appl
15	484.5	38.1	740	14	US-10-167-015-7	Sequence 7, Appl
16	483.5	38.0	2922	9	US-09-925-302-73	Sequence 73, Appl
17	483.5	38.0	2994	13	US-10-044-090-356	Sequence 356, Appl
18	426	33.5	376	10	US-09-878-574-1827	Sequence 1827, Ap
19	422	33.2	308	14	US-10-167-015-22	Sequence 22, Appl
20	371.5	29.2	536	10	US-09-998-598-1405	Sequence 1405, Ap
21	339	26.7	234	14	US-10-167-015-19	Sequence 19, Appl
22	301	23.7	529	12	US-10-002-631C-3	Sequence 3, Appl
23	296	23.3	251	10	US-09-878-574-7224	Sequence 7224, Ap
24	285	22.4	410	10	US-09-960-352-8444	Sequence 8444, Ap
25	280	22.0	803	14	US-10-167-015-21	Sequence 21, Appl
26	255	20.0	257	10	US-09-878-574-6304	Sequence 6304, Ap
27	219	17.2	392	10	US-09-960-352-8713	Sequence 8713, Ap
28	219	17.2	431	10	US-09-960-352-13324	Sequence 13324, A
29	193.5	15.2	250	9	US-09-923-876-298	Sequence 298, App
30	189	14.9	415	11	US-09-918-995-36866	Sequence 36866, A
31	188	14.8	601	11	US-09-871-161-231	Sequence 231, App
32	184	14.5	422	11	US-09-918-995-16385	Sequence 16385, A
33	165	13.0	1316	12	US-10-177-023-1	Sequence 1, Appli
34	165	13.0	1355	11	US-09-822-846-122	Sequence 122, App
35	165	13.0	1394	9	US-09-745-763-67	Sequence 67, Appl
36	165	13.0	1596	11	US-09-809-391-184	Sequence 184, App
37	165	13.0	1943	9	US-09-989-722-1	Sequence 1, Appli
38	165	13.0	1943	9	US-09-989-723-1	Sequence 1, Appli
39	165	13.0	1943	9	US-09-989-279-1	Sequence 1, Appli
40	165	13.0	1943	9	US-09-989-727-1	Sequence 1, Appli
41	165	13.0	1943	10	US-09-989-731-1	Sequence 1, Appli
42	165	13.0	1943	10	US-09-989-732-1	Sequence 1, Appli
43	165	13.0	1943	10	US-09-991-073-1	Sequence 1, Appli
44	165	13.0	1943	10	US-09-990-442-1	Sequence 1, Appli
45	165	13.0	1943	10	US-09-991-163-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-955-526-3
; Sequence 3, Application US/09955526
; Publication No. US20030009785A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Plant Cytoprotective Genes and Methods
; FILE REFERENCE: of Using Same
; FILE REFERENCE: P-LJ 4668
; CURRENT APPLICATION NUMBER: US/09/955,526
; PRIOR FILING DATE: 2001-09-12
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1034
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (87)...(830)
; NAME/KEY: misc.feature
; LOCATION: (1)...(1034)
; OTHER INFORMATION: n = A,T,C or G

US-09-955-526-3

Alignment Scores:

Pred. No.: 4,38e-152 Length: 1034
Score: 1272.00 Matches: 248
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-955-526-4 (1-248) x US-09-955-526-3 (1-1034)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTyrSerTyr 20
DB 87 ATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCTCTCGCAACCGTGGAGTTAT 146
QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
DB 147 GATTCCTCAAAAACCTCCGCCAGATCTCACCTCTCGTTCAACTCATCTCAAGCAGGTG 206
QY 41 TyrLeuThrLeuLysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
DB 207 TACCTTAGGCTATGCTGTCTTAGTGGCATGGCTGTGGGGCTTACCTTCACATTTCTA 266
QY 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTyrLeuLeu 80
DB 267 TGGAAATATCGGTGGCTCTCTCAACAATGGCTTCGATGGGAGCATGGTGTGGCTTCTC 326
QY 81 SerAlaProTyrGlnGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
DB 327 TCAGCTCCTCCTTATCAAGAGCAAAAAGGTGGCTCTCTCATGGCAGCTGCATTTT 386
QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
DB 387 GAAGCGCGCTCTATGGTCTCTGATGAGCTGGGCAATTAATTCGATCCAGCATTTGG 446
QY 121 PheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaAlaMetLeu 140
DB 447 TTTGGCGCTTTGTAGTTGTGCTGGTTTGGTTTGGTTCTCTCAGCTGCTGCCATGTTG 506
QY 141 AlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
DB 507 GCAAGCGCAGGAGTACTTGTACCTCGGGGGCTCTTTCTATCTGGCTCTCCCTTCTC 566
QY 161 PheTrpLeuHisPheAlaSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180
DB 567 TTCCTGGTGCACCTTGCATCCCTCCATTTTGGTGGTTCATGCTGTTTTCAGTTTGA 626
QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIle 200
DB 627 TTGTATTTTGGACTCTTGGTGTGTGTGGCTACATGCTTTTGACACCCCAAGAAATTA 686
QY 201 GluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThr 220
DB 687 GAGAAGGCTACCTTGGGTGATAGGATACGTTAAGCATGCAATGACCTTTTCACAGAT 746
QY 221 PheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGluLysGlu 240
DB 747 TTTGGCGCTTTTTCGGCGATCTTCATCATCATCTTAAAGAAATGCACTGAGAGGAA 806
QY 241 GluLysLysLysLysArgAsn 248
DB 807 GAGAAGAAGAAGAAGAGGAGAAAC 830

RESULT 2

US-09-770-445-223

; Sequence 223, Application US/09770445
; Patent No. US2002023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorchach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.

; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Ted
; APPLICANT: Slader, Maja
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurdan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 1009
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-770-445-223
Alignment Scores:
Pred. No.: 6,22e-121 Length: 1009
Score: 1027.50 Matches: 193
Percent Similarity: 90.32% Conservatives: 31
Best Local Similarity: 77.82% Mismatches: 23
Query Match: 80.78% Indels: 1
DB: 9 Gaps: 1
US-09-955-526-4 (1-248) x US-09-770-445-223 (1-1009)
QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTyrSerTyr 20
DB 38 ATGGAATGCGTTCCT 94
QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
DB 95 GATTCCTTAAAAACCTTCGCTCAGATTTCTCCAGCGGTTTCAGAAATCATCTTAAACGG 154
QY 41 TyrLeuThrLeuLysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
DB 155 TATTTGACCTTATGTTGCT 214
QY 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTyrLeuLeu 80
DB 215 TGAATATCGCGGTATCTTTCACAGCATTTGATGATTTGGAACTATGATTTGGCTCTT 274
QY 81 SerAlaProTyrGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
DB 275 TCATGCTCTCTTATGACACCAAAAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 334
QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
DB 335 GAAGTGTCTTCTGTTGGCCCTTGATCAAAAGTGGCAATGATGTTGCTTCTCTCTCTCT 394
QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeu 140
DB 395 ATCAGTTCGCTTGTGGACTGGATAGCGTTTGTCTCTCTCTCTCTCTCTCTCTCTCT 454
QY 141 AlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
DB 455 GCAAGACGACGAGGATCTCTACCTTGGAGGACTGCTTCTCTCTCTCTCTCTCTCT 514
QY 161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180

QY	84	ProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPheGluGlyAla	103
Db	238	CGTTTGTGAAGAGAGAGAGGTCACCTTTGTGTGATGGCCGCTACCTACTGTTTCAGGCGTCC	297
QY	104	SerIleGlyProLeuIleGluLeuGlyTleAsnPheAspProSerIleValPheGlyAla	123
Db	298	TCATATGGACCCTTGATGTGATTTGGCTATTCAATCGATCCAGCCCTATCTTTAGTGCA	357
QY	124	PheValGlyCysAlaValAlaValPheGlyCysPheSerAlaAlaMetLeuAlaArgArg	143
Db	358	TTTGTGGGAACAGCTTTGGCTTTGCATGCTTCTCAGGACGAGCTTTGGTTGCAAGCGT	417
QY	144	ArgGluTyrLeuTyrLeuGlyCysLeuLeuSerSerGlyValSerLeuLeuPheTyrLeu	163
Db	418	AGGGAGTACCTGATCCTTGGTGGCTTGGTTTCTTCTGGATTTGCCCTCTCTGGTTG	477
QY	164	HisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGluLeuTyrPhe	183
Db	478	CACCTTTGCTCTCCATCTTTGGAGGCTCAACAGCTCTCTCTTAAGTTTGAGTTGTACTTT	537
QY	184	GlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleIleGluLysAla	203
Db	538	GGGCTATTGGTGTTGTAGGTACATTGTAGTAGACACCCCAAGAAATAGTTGAGAGGGCA	597
QY	204	HisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAla	223
Db	598	CACTTGGGGGATCTGGACATGTAAAGCATGCCCTTGACCTTGTTTACCGATTTGGTCGCA	657
QY	224	ValPheValArgIleLeuIleIleMetLeuLysAsnAlaSerGluLysGluGluLysLys	243
Db	658	GTTTGTTCGGATTCCTGTTATTATGTTGAAGAATTCGACTGAGAGGAATGAGAGAAA	717

97

184	GlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleIleGluLysAla	203
538	GGGCTATTGGGTCTTTTGTAGTTACATTGTAGTACACACCCCAAGAAATAGTTGAGAGGGCA	597
204	HsLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAla	223
598	CACCTTGGGGGATCTGGCATGTGAAGCATGCCCTTGACCTTGTTTACCGATTTGGTCGCA	657
224	ValPheValArgIleLeuIleIleMetLeuLysAsnAlaSerGluLysGluGluLysLys	243
658	GTTTTTCGGGATCTCTGTATTATGTTGAAGAATTCGACTGAGAGGAATGAGAGAAA	717
244	LysLysArgArgAsn	248
718	AAGAAGAGAGAAGAT	732
RESULT 4		
US-10-219-220-232		
; Sequence 232, Application US/10219220		
; Publication No. US20030082724A1		
; GENERAL INFORMATION:		
; APPLICANT: Flino, Barry		
; APPLICANT: Lasham, Annette		
; TITLE OF INVENTION: Compositions affecting programmed cell		
; TITLE OF INVENTION: death and their use in the modification of plant develo		
; FILE REFERENCE: 11,000,1023		

CURREN;
CURREN

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; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 1218

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TYPE	ORGAN
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US-10-219-220-232

Alignment Scores:
Pred. No.:          Length:      1218
Score:              Matches:      186
                    Conservative:  27
Percent Similarity: 85.20%
Best Local Similarity: 74.40%
                    Mismatches:    32
Query Match:       75.75%
                    Indels:        5
DB:                Gaps:          2
                    14

US-09-955-526-4 (1-248) x US-10-219-220-232 (1-1218)

Qy      1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
      |||:: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      123 ATGGACGGGTTCGCTTCCTCTCCAGTCG-----AGCGGCAAGGGGTGGAGCCAC 173

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aSerArgAsnArgTrpSerTyr 20
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-AGCGGCAAGGGTGGAGCCAC 173
lglnThrHisLeuLvsGlnVal 40

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174 GATTCCTCAAGAACTTCGCGCAGATATCTCCGCGCTCCCAATCTCACTCAAGAAATGTT 233
QY
41 TyrLeuThrLeuCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
|||||
234 TATCTGCTTATGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 293
Db
61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
|||||
294 CTGAACATCGCGGCTCTCTCAGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 353
Db
81 SerAlaProProTyrGlnGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
|||||
354 TCGATCTCTCAGATGAGAGAAAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 413
Db
101 GluGlyAlaSerIleGlyProLeuLeuGlnLeuGlyIleAsnPheAspProSerIleVal 120
|||||
414 GAAGGAGCGTGTATTGCTCTCTCATGACGCGGCCATTAAAGGTGAGCCGAGCATTTG 473
Db
121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeu 140
|||||
474 ATAAGCGCATTTGTTGGGATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
Db
141 AlaArgArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeu 160
|||||
534 GCTAGCGGAGGAGTACCTATATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
Db
161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180
|||||
594 ATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 653
Db
181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIle 200
|||||
654 ATATATCTTTGGGCTTTTATGTTCTATCGGCTATGCTGCTGCTGCTGCTGCTGCTGCT 713
Db
201 GluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAsp 220
|||||
714 GAGTAGCACACACAGGAGTATGACATGATGTAAGCATTCGTTGAACCTCTTCACTGAT 773
Db
221 PheGlyAlaValPheValArgIleLeuIleLeuMetLeuLysAsnAlaSerGluLysGlu 240
|||||
774 TTCGTGGCTATTTTGTCCGAATCTCATCATCATGCTGCTGCTGCTGCTGCTGCTGCT 833
Db
241 -----GluLysLysLysLysArgArgAsn 248
QY
834 AAGAACGAGAGAGAGAGAGAGAGAGAT 863
Db
```

RESULT 5

```
US-10-167-015-17
; Sequence 17, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yimin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37)...(822)
```

US-10-167-015-17

```
Alignment Scores:
Pred. No.: 1,05e-111 Length: 989
Score: 955.00 Matches: 178
Percent Similarity: 88.07% Conservative: 36
Best Local Similarity: 73.25% Mismatches: 27
Query Match: 75.08% Indels: 2
DB: 14 Gaps: 1
```

US-09-955-526-4 (1-248) x US-10-167-015-17 (1-989)

```
QY 6 SerPhePheAspSerGln-----SerAlaSerArgAsnArgTrpSerTyrAspSerLeu 23
Db
43 ACCCTTCTCAATCTCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 102
QY 24 LysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeuThr 43
Db
103 AAGAAATTCCTGAGATCTCTCCGCTGCTTCCAGATCATCAACAGGGGTTATTTTACG 162
QY 44 LeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsnIle 63
Db
163 TTATGTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 222
QY 64 GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaPro 83
Db
223 GGGGTTTCTCACCACCGTTGCCATTTGGAACATGGTTTGGTTGCTATCTACACC 282
QY 84 ProTyrGlnGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPheGluGlyAla 103
Db
283 CTTGTTGAAGACAAAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 342
QY 104 SerIleGlyProLeuLeuGlnLeuGlyIleAsnPheAspProSerIleValPheGlyAla 123
Db
343 TCCATTTGACCTCTCATTTGCTATTTGCTATTTGCTATTTGCTATTTGCTATTTGCTAT 402
QY 124 PheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeuAlaArgArg 143
Db
403 TTTTGGGCAACTCTTTGCTTTTGGCTTTTGGCTTTTGGCTTTTGGCTTTTGGCTTTTGG 462
QY 144 ArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeuPheTrpLeu 163
Db
463 AGGGAGTACCTCTACCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 522
QY 164 HisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGluLeuTyrPhe 183
Db
523 CACTTTGCTCTCTCTCTTTGGGGCTCAATTCACICTTCAAGTTTGAGCTGTACITTT 582
QY 184 GlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleLeuLysAla 203
Db
583 GGGCTTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 642
QY 204 HisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAla 223
Db
643 CACTTTGGTACCTGGATTTATGTGAAGCATGATGACATTTGTCATGATTTGGTGTCA 702
QY 224 ValPheValArgIleLeuIleLeuMetLeuLysAsnAlaSerGluLysGluLysLys 243
Db
703 ATCTTTGTCCGAATCTTATTAATGTTGAAGAAATTCATTTTGGGGGAAATGGGAAGAAG 762
QY 244 LysLysArg 246
Db
763 AAGAAAAGG 771
```

RESULT 6

```
US-10-167-015-31
; Sequence 31, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
```

```

; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 1026
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (72)...(830)
US-10-167-015-31

Alignment Scores:
Pred. No.: 1,08e-102 Length: 1026
Score: 884.50 Matches: 166
Percent Similarity: 80.80% Conservative: 36
Best Local Similarity: 66.40% Mismatches: 41
Query Match: 69.54% Indels: 7
DB: 14 Gaps: 2

US-09-955-526-4 (1-248) x US-10-167-015-31 (1-1026)

QY 6 SerPheAspSerGlnSerAlaSer-----ArgAsnArgTrpSer 19
Db GCCTTCCTCGGGTCCCTCGCGGTGGCGGCCCTACGGGTACGGCGCGCGAGTGAGC 137

QY 20 TyrAspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGln 39
Db TACGACTGCTCAAGAACTTCGCAGATCACCCCCTCGTCCAGACCACCTCAAGCTC 197

QY 40 ValTyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIle 59
Db GTCTACTCATCCCTGTGCGCGCGCTGCTGCGCGGTGGCGCTTACCTGCACGCTG 257

QY 60 LeuTrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeu 79
Db GTCTGAACAATCGCGGTACGTGACAATGCTGGTTGCTGCGGAGCATCGCCCTGGCTC 317

QY 80 LeuSerAlaProTyrGlnGluInLysArgValAlaLeuLeuMetAlaAlaLeu 99
Db TTCTCGGTGCCCCCTACGAGGAGAGAGAGATGAGTGGCTGCTGATGGCGCTGCCCTC 377

QY 100 PheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIle 119
Db CTGGAAGGCGCTTCGTGCGGACCCCTCGTCAAGCTCGCGTGGAAATTGACCCAAGCATC 437

QY 120 ValPheGlyAlaPheValGlyCysAlaValAlaValPheGlyCysSerAlaAlaMet 139
Db CTGCTGAGCGCTTCGTGGGACTGCATCGCGTTCGCTGCTTACCGCGCGGCGCATG 497

QY 140 LeuAlaArgArgGluTyrLeuTyrLeuGlyIleLeuSerSerGlyValSerLeu 159
Db GTGCGCAGGCGCAGGAGTACCTTACCTGGGTGGCTGCTCTGCTGGGGCTCTCCATC 557

QY 160 LeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPhe 179
Db CTGCTCTGGCTGACGTAGCGGCTGCATCTTCGGCCACTCGCAACACCATGCTCATGTTC 617

QY 180 GluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIle 199
Db GAGCTTACTTCGGGCTGCTCACTTCCTGGGGTAGCTGTTGACACACGAGAGATC 677

QY 200 IleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThr 219
Db ATCAGAGGCGGACCGCGCGCATGGACCATGACCATGCTCAACACGCGCTTCCCTTTCACA 737

```



```

Percent Similarity: 80.00%      Conservative: 36
Best Local Similarity: 65.60%   Mismatches: 43
Query Match: 68.47%            Indels: 7
DB: 14                          Gaps: 1

US-09-955-526-4 (1-248) x US-10-167-015-3 (1-1026)

QY 6 SerPhePheAspSerGlnSerAlaSer-----ArgAsnArgTrpSer 19
Db 78 GCGTTTCTTCGCGCTCCCTCCGCGTCCGCGCCCTACGGCTACGGCGCGCGGATGGAGC 137

QY 20 TyrAspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGln 39
Db 138 TAGCACTCGCTCAAGAACTTCGCGCAGATCACCCCGCGCTCCAGACCACCTCAAGCTC 197

QY 40 ValTyrLeuThrLeuLysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisTle 59
Db 198 GTTACTCTCACCCTGTCGCGCGCTGGCGCTGCTCGCGCTGGCGCTTACCTGCACGCTG 257

QY 60 LeuTrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeu 79
Db 258 GTCTGGACATCGCGGCTAGCTGACAAATGCTCGGTGCTCGGAGATCATCCCTGGCTC 317

QY 80 LeuSerAlaProProTyrGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeu 99
Db 318 TTCTCGGTGCGCTCACGAGAGAGAGATGATGGCTGCTGATGGCGCTGCCCTC 377

QY 100 PheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIle 119
Db 378 CTGAGAGGCTCTGCTGCGACCCCTGCTCAAGCTCGCGTGGAAATTCACCAAGCATC 437

QY 120 ValPheGlyAlaPheValGlyCysAlaValAlaPheGlyCysPheSerAlaAlaMet 139
Db 438 CTGGTACGCGCTCTGCGGACTGCTATCGCTTCTGCGTCTCACCGCGCGGCCATG 497

QY 140 LeuAlaArgArgGlnTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeu 159
Db 498 GTGGCCAGCGCAGGAGATCTCTACCTCGGTGGGCTGCTCTCGTGGGCTCTCCATC 557

QY 160 LeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPhe 179
Db 558 CTGCTCTGGCTGACGTACGCGCTCCATCTTCGCGCATCTCGCAACCATCTCATGTC 617

QY 180 GluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluLe 199
Db 618 GAGTCTACTTCGGGTGCTCATCTCTCCGCTAGGTGCTGCTGCTGCTGCTGCTGCTGCT 677

QY 200 IleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThr 219
Db 678 ATGAGAGGCGCACCGCGCGCACATGGACACCGCTCAACGACCGCTCATCTCTCACA 737

QY 220 AspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGluLys 239
Db 738 GACTCTGTCGCGCTCTCTGCGCGCTCTCTGCGCTCTCTGCGCTCTCTGCGCTCTCTG 797

QY 239 sGluGluLysLysLysLysArgArgAsn 248
Db 798 GTCGGAGGACAGAGAGAGAGAGAGAGT 825

RESULT 10
US-10-167-015-1
; Sequence 1, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarrio
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015

```

Db 632 CGGATTTACACATTTGAGATCTACTCGGCTGCTAGTTTTCCCTGGGTATATATATTT 691
 Qy 195 AspThrGlnGluIleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAla 214
 Db 692 GACACACAGATGATCATCGAGAAAGCGGACCATGGAGACTATGATTATTTAAACATTTCA 751
 Qy 215 LeuThrLeuPheThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLys 234
 Db 752 CTGACCTCTTCATGTACTTCGTTGCTGTATTTGTTCCCTCATGGTCATATATGCAAG 811
 Qy 235 AsnAla---SerGluLysGluGluLysLysLysLysArgArg 247
 Db 812 AATGCACACAGTAATCCAGGGAAGGAAAAAGAGGAAGG 853
 RESULT 12
 US-10-219-220-43
 ; Sequence 43, Application US/10219220
 ; Publication No. US20030082724A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Flinn, Barry
 ; APPLICANT: Lasham, Annette
 ; TITLE OF INVENTION: Compositions affecting programmed cell
 ; TITLE OF INVENTION: death and their use in the modification of plant development
 ; FILE REFERENCE: 11000.1022c1
 ; CURRENT APPLICATION NUMBER: US/10/219,220
 ; CURRENT FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
 ; PRIOR FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 290
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 43
 ; LENGTH: 884
 ; TYPE: DNA
 ; ORGANISM: Pinus radiata
 US-10-219-220-43
 Alignment Scores:
 Pred. No.: 8.35e-78 Length: 884
 Score: 688.50 Matches: 137
 Percent Similarity: 79.25% Conservative: 31
 Best Local Similarity: 64.62% Mismatches: 41
 Query Match: 54.13% Indels: 3
 DB: 14 Gaps: 2
 US-09-955-526-4 (1-248) x US-10-219-220-43 (1-884)
 Qy 39 GlnValTyrLeuThrLeuCysCysAlaLeuValAlaSerAlaIleGlyAlaTyrLeuHis 58
 Db 2 AGSGTTTATTTGCTCGTTAGCTGTGCCCTGCTAACAGCAGCATCGGTGTTTATTTCAT 61
 Qy 59 IleLeuTrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrp 78
 Db 62 CTTCGTGTGAATATGTGAGGCTCTCACGGGGGCTCGCTGCATGGTGTCTGTAATCGGG 121
 Qy 79 LeuLeuSerAlaPro-----ProTyrGlnGlnLysArgValAlaLeuLeuMetAla 96
 Db 122 CTCCTATCCGTCCTACTCTCTCGAACAAATCAGGGTAGAGAGCTGCCTGCTCTGGCA 181
 Qy 97 AlaAlaLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAsp 116
 Db 182 GCTCCTCGCTCAAGGGAGCTACTCTGGACCGCTCATCGACGGGTCAATTAATTTGAC 241
 Qy 117 ProSerIleValPheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAla 136
 Db 242 TCCAGTATACCTGGTGTGCGTTTGTGGGACCTCTTTGGCCTTCGCTTTCGCGCA 301
 Qy 137 AlaAlaMetLeuAlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGly 156
 Db 302 GCACCAATCACAGCCAGGAGCGGAATACCTATTTTGGGAGGATTTATGGGCTCGGGA 361
 Qy 157 ValSerLeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaVal 176
 Db 362 ATCAGCATATTGATGTGGCTGCAACTAGCATCCTGATTGTTGGTGTCTTCGCGCAT 421

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QY 177 PheLysPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThr 196
Db 422 TACACATTTGAGATCTACTTCGGTCTGCTAGTTTCTTGGGTATATTATATTGACACA 481
QY 197 GlnGluIleGlyLeuLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThr 216
Db 482 CAGATGATCATCGAAGAGCGGACCATGGAGACTATGATTATTAAACATTCCTCTGGAC 541
QY 217 LeuPheThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAspAla 236
Db 542 CTCCTTCATTCGTCGTGCTGTATTTGTCGCTGATGTCATTAATGGCAAGATGCA 601
QY 237 ---SerGluLysGluGluLysLysLysArgArg 247
Db 602 GACAGTAATCCAGGSAAGGAAAAAGAGAAG 637

RESULT 13
US-10-219-220-44
; Sequence 44, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-219-220-44

Alignment Scores:
Pred. No.: 4,71e-54 Length: 527
Score: 499.50 Matches: 101
Percent Similarity: 79.72% Conservative: 13
Best Local Similarity: 70.63% Mismatches: 26
Query Match: 39.27% Indels: 4
DB: 14 Gaps: 1

US-09-955-526-4 (1-248) x US-10-219-220-44 (1-527)
QY 1 MetGluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
Db 107 ATGAGCGGTTCGTYCCCTGTTCCAGTCG-----AGCGGAAGGGGTGGAGCCAC 157
QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
Db 158 GATTTCCTCAAGAACTCCGCCAGATATCTCCGCCGTCACCTCAACCTCAAGATGTT 217
QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaGlyAlaTyrLeuHisIleLeu 60
Db 218 TATCTGCTTATGCTGTGCTGTATGCTTCGGCGGTTCGGCGGTTCGCTTACCTGCATCTGATG 277
QY 61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 278 CTGACATCGCGGGCTCTCCAGACAAATTCCTTGCATCGAAGCATTCGTGGCTGCTT 337
QY 81 SerAlaProProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
Db 338 TCGATTCTCCACATGAAGAGCAAGAGGTTTGGTCTGCTCATGGCGGCGGCTCTCTT 397
QY 101 GlucylAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
Db 398 GAAGGACGCGTATCTCGCTCTCTCATCGAAGCGGCCCATTAAGGTTCGAGCGCATTTGTG 457

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QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetIleu 140
Db 458 ATAAGCGCATTTGGGATCTGCGCTGCGCTTCTGCTTCTCGGGGCGCAGC-ATGTTG 516
QY 141 AlaArgArg 143
Db 517 GCTAGCGCG 525

RESULT 14
US-10-263-828-6
; Sequence 6, Application US/10263828
; Publication No. US20030138903A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: mammary gland and methods for their use.
; FILE REFERENCE: 11000.1044U1con
; CURRENT APPLICATION NUMBER: US/10/263,828
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Bovine
US-10-263-828-6

Alignment Scores:
Pred. No.: 1.06e-52 Length: 873
Score: 491.50 Matches: 99
Percent Similarity: 65.80% Conservative: 53
Best Local Similarity: 42.86% Mismatches: 72
Query Match: 38.64% Indels: 7
DB: 12 Gaps: 4

US-09-955-526-4 (1-248) x US-10-263-828-6 (1-873)
QY 19 SerTyrAspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLys 38
Db 55 AACTTTGATGCATCTTTAAATTTCCACATATACCCCTCGACACAGCAGCCTGAAG 114
QY 39 GlnValTyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHis 58
Db 115 AAGTTTATGCCAGTTTTCCTCTGTATGTTTGTGGCGCTGCGGGGCGCTATATCAT 174
QY 59 IleLeuTrpAsnIle-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMet 76
Db 175 GTGGTACCCCATTTTCATTCAGGCTGGCTGCTCTCTGCTTGGGCTCTTTGGGTTGATG 234
QY 77 ValTrpLeuLeuSerAlaProTyrGln-----GluGlnLysArgValAlaLeuLeu 94
Db 235 ATTTGGCTGATGGCAACACCTCACAGCCATGAACACTGAGCAAAAAGACATGGGACTCTG 294
QY 95 MetAlaAlaLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsn 114
Db 295 GCTGGAFTTCTTCCTTACAGGAGTTGGCTGGCCCTGCTGGACTTGTGCATTGCC 354
QY 115 PheAspProSerIleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPhe 134
Db 355 ATCAACCCAGCATTCCTCCACTGCTTCATGGGACAGCAATGATCTTCACCTGCTTC 414
QY 135 SerAlaAlaAlaMetLeuAlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSer 154
Db 415 ACCCTGAGTGCATCTATGCGAGCGCGCTAGTACTCTCTTCTAGAGAGTATCTTGATG 474
QY 155 SerGlyValSerLeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMet 174
Db 475 TCGGCCATGAGCCTCATGCTC---TTGTCTCCCTGGGGAACCTTTTCTTCGGATCNGTT 531
QY 175 AlaValPheLysPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPhe 194

```

```
Db 532 TGCGTTTTCAGCAACCTGTATATGGGCTGTGTGTCATGTCGTGGCTTTGTCCTTTT 591
QY 195 AspThrGlnGluLeuIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAla 214
Db 592 GATACCTCACTCATTTGAAAGGCTGAATGGAGATAAAGATTTATATCTGGCACTGC 651
QY 215 LeuThrLeuPheThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLys 234
Db 652 GTTGACCTCTCTGTGGATTTCGTAACCTCTTCAGAAAGCTCATGATGATCCTGGCTATG 711
QY 235 AsnAlaSerGluLysGluGluLysLysLysLys 245
Db 712 AAT-----GAGAGGATAGAGAGAGAGAG 738
```

RESULT 15

```
US-10-167-015-7
; Sequence 7, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 740
; TYPE: DNA
; ORGANISM: zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(489)
US-10-167-015-7
```

Alignment Scores:

Pred. No.:	6,46e-52	Length:	740
Score:	484.50	Matches:	93
Percent Similarity:	82.61%	Conservative:	21
Best Local Similarity:	67.39%	Mismatches:	23
Query Match:	38.09%	Indels:	1
DB:	14	Gaps:	1

US-09-955-526-4 (1-248) x US-10-167-015-7 (1-740)

```
QY 112 GlyIleAsnPheAspProSerIleValPheGlyAlaPheValGlyCysAlaValValPhe 131
Db 73 GGCTGTTTTTTTCCCTCAGCATCTGTGTGACGGCGTTCGTGGGACTGCCATCGCGTTC 132
QY 132 GlyCysPheSerAlaAlaAlaMetLeuAlaArgArgGluTyrLeuTyrLeuGlyCly 151
Db 133 GCGTGCCTTCACCGCGCGGCATGGTGCCACAGCGGAGTACCTCTACCTGGGTGG 192
QY 152 LeuLeuSerSerGlyValSerLeuLeuPheTrpLeuHisPheAlaSerSerIlePheGly 171
Db 193 CTGCTCTCGTGGGGCTCTCCATCTGCTGTGCTGAGCTAGCGGCTCCATCTCTGGC 252
QY 172 GlySerMetAlaValPheLysPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyr 191
Db 253 CACTCGCAACACAGCTTCATGTCGAGGTCTACTTCGGGCTGCTCATCTCTGGGCTAC 312
QY 192 IleValPheAspThrGlnGluIleGluLysAlaHisLeuGlyAspMetAspTyrVal 211
Db 313 GTGTGTACGACGACGAGAGATCATCGAGAGGCGCACCGCGGCGAGATGGACACGTC 372
```

```
QY 212 LysHisAlaLeuThrLeuPheThrAspPheGlyAlaValPheValArgIleLeuIle 231
Db 373 AAGCAGCCCTCACCTCTTTCACAGACTTCGTGGCCGCTCTCGCTCGCTCGTCAIC 432
QY 232 MetLeuLysAsnAlaSerGluLys---GluGluLysLysLysLysLysArgArgAsn 248
Db 433 ATGCTCAGAACCGGGGCCGACAAAGTCGGAGGACAAAGAGAGAGAGAGAGAGTCG 486
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Search completed: September 22, 2003, 17:53:08

Job time : 251 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 22, 2003, 15:28:24 ; Search time 2060 Seconds
(without alignments)
2925.976 Million cell updates/sec

Title: US-09-955-526-4
Perfect score: 1272
Sequence: 1 MEGFTFFDSQASRNWSY.....LIIMLNASEKEKKRRN 248

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n_model -DEV=xlp
-O=/cgn2_1/USPTO_spool/US0955526/runat_22092003_151755_12377/app_query.fasta.1.391
-DB=EST_QFMT-fastp -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEPAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0955526 -CGN 1.1 4237 @runat_22092003_151755_12377 -NCPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmd:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1088.5	85.6	750	10	BG124317
2	1042	81.9	655	12	BM066817
3	1032	81.1	757	14	CA811916
4	1020	80.2	596	9	AI779122
5	1016	79.9	732	13	BU023368
6	1012	79.6	706	14	CB978248
7	990	77.8	739	13	BU895008
8	961	75.6	671	12	BI933489
9	960	75.5	643	9	AW096641
10	947	74.4	646	9	AW219279
11	940	73.9	831	12	BG839316
12	933	73.3	723	13	BO856331
13	932	73.3	647	10	BG127849
14	931	73.2	691	13	BU896719
15	931	73.2	694	13	BU867362
16	927	72.9	713	13	BQ991270
17	914	71.9	703	13	BO863266
18	888	69.8	643	14	CA812546
19	888	69.8	726	10	BG648712
20	879.5	69.1	738	14	CB293933
21	878.5	69.1	647	10	BE577220
22	871	68.5	694	10	BG646982
23	871	68.5	1096	11	AY105656
24	870	68.4	671	14	CA825814
25	866	68.1	611	13	BU836328
26	865	68.0	592	10	BG134507
27	862	67.8	608	14	CA823531
28	858	67.5	578	13	BQ115430
29	855	67.2	626	14	CA847592
30	851	66.9	696	14	CA909307
31	846	66.5	611	12	BJ554597
32	845	66.4	590	12	BM082213
33	844	66.4	680	14	CA909308
34	843	66.3	646	14	CB347734
35	842	66.2	611	12	BJ560791
36	840	66.0	593	12	BM062746
37	840	66.0	748	13	BU100498
38	838	65.9	620	9	AI730983
39	837	65.8	621	9	AI728851
40	836.5	65.8	700	14	CD038782
41	835	65.6	619	9	AI727198
42	835	65.6	643	14	CB894392
43	834	65.6	740	13	BQ255427
44	832	65.4	681	10	BF635314
45	828	65.1	776	10	BG648573

ALIGNMENTS

RESULT 1
BG124317
LOCUS
DEFINITION
EST469963 tomato shoot/meristem Lycopersicon esculentum cDNA clone
ctof4l8 5' sequence, mRNA sequence.
ACCESSION
BG124317
VERSION
BG124317.1
KEYWORDS
EST.
GI:12624505
ORGANISM
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 750)
 AUTHORS van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T., Hansen, C., Ronning, C. and Tanksley, S.
 TITLE Generation of ESTs from tomato shoot/meristem tissue
 JOURNAL Unpublished
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES
 source
 1..750
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cTOF418"
 /tissue_type="shoot/meristem"
 /dev_stage="developing shoots from 4-6wks old plants"
 /lab_host="SOLR"
 /clone_lib="tomato shoot/meristem"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
 BASE COUNT 158 a 174 c 176 g 242 t
 ORIGIN

Alignment Scores:
 Pred. No.: 8,68e-94 Length: 750
 Score: 1088.50 Matches: 214
 Percent Similarity: 98.17% Conservative: 0
 Best Local Similarity: 98.17% Mismatches: 3
 Query Match: 85.57% Indels: 1
 DB: 10 Gaps: 1

US-09-955-526-4 (1-248) x BG124317 (1-750)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
 DB 95 ATGGAAGGTTTCACATCGTCTTCGACATCGCAATCGCTCTCGCAACGGCTGGAGTTAT 154

QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
 DB 155 GATTCCTCAAAAATCTCCGGCAGATCTCACCTCTCGTTCAAACATCACTCAAGCAGGTG 214

QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
 DB 215 TACCTTAGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGCTTACCTTCACATTCTA 274

QY 61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
 DB 275 TGGAAATCGGTGGCTCTCCACAAATGGCTTCATGGGAAGCATGGTGTGGCTTCTC 334

QY 81 SerAlaProProTyrGlnGlu---GlnLysArgValAlaLeuLeuMetAlaAlaLeu 99
 DB 335 TCAGCTCCTCTATCAGAGCAGCAAAAAGGGTGGCTCTCTGATGGCAGCTGCATT 394

QY 100 PheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIle 119
 DB 395 TTGGAAGCGGCTCTATTGGTCTCTGATTTAGTGGTGGTCTTCTGATGGCAGCTGCATT 454

QY 120 ValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMet 139
 DB 455 GGTGTTGGCGCTTTGTAGGTGTGCTGTGTTTGTGTTGCTTCTGATGGTGGTGGTGGT 514

QY 140 LeuAlaArgArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeu 159
 DB 515 TTGGCAAGCGCAGGAGTACTTGACCTCGGGGCGCTCTCTTCTATCTGGGCTCTCCCTT 574

QY 160 LeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPhe 179
 DB 575 CTCCTCTGGTTCACCTTTGCATCCCTCCATTTTGTGTTGCTTCCATGGCTTTTCAAGTTT 634

QY 180 GluLeuTyrPheGlyLeuValPheValGlyTyrIleValPheAspThrGlnGluIle 199
 DB 635 CAGTTGTATTGGACTCTTGGGTCTTGGGCTACATCGTCTTTGACACCAAGAAAT 694

QY 200 IleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeu 217
 DB 695 ATTGAGAAAGCTCACTTGGGTGATATGGATTACGTTAAGCATGCAATTGACCTT 748

RESULT 2
 BM066817 1..655
 LOCUS BM066817 KS07 Capsicum annum cDNA, mRNA linear EST 11-SEP-2002
 DEFINITION BM066817
 ACCESSION BM066817
 VERSION 1
 KEYWORDS EST.
 SOURCE Capsicum annum
 ORGANISM Capsicum annum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 655)
 AUTHORS Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G. and Choi, D.
 TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
 JOURNAL Unpublished
 COMMENT Contact: Doil Choi
 Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doilemail.kribb.re.kr
 High quality sequence stop: 655.

FEATURES
 source
 1..655
 /organism="Capsicum annum"
 /mol_type="mRNA"
 /cultivar="Hang Keun"
 /db_xref="taxon:4072"
 /tissue_type="flower bud"
 /dev_stage="10 weeks after germination"
 /clone_lib="KS07"
 /note="Vector: Hydri-ZAP 2.1"
 BASE COUNT 124 a 160 c 161 g 210 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2.06e-89 Length: 655
 Score: 1042.00 Matches: 198
 Percent Similarity: 96.74% Conservative: 10
 Best Local Similarity: 92.09% Mismatches: 7
 Query Match: 81.92% Indels: 0
 DB: 12 Gaps: 0

US-09-955-526-4 (1-248) x BM066817 (1-655)

QY 2 GluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAsp 21
 DB 9 CAGGGTTTCAGTCTGCTTCGATCGCAATCGGCTTCGCGAGCTCGTGAATATGAT 68

QY 22 SerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyr 41
 DB 69 GCTCTCAAAAATCTCCATCATCATCTCTCTCGTGTTCAAACTCATCTCAACAGCTTAC 128

QY 42 LeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrp 61
 DB 129 CTCACATATCTGTGCTTTAGTCGATCAGCTGCTGGGCTTACCTTCACATTCTTGG 188

QY 62 AsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeuSer 81
 DB 188

Db 189 AACATCGGTGGCTTCTCACACACTGGCTTCATTTGGAAGCATGGTGGCTTGGCA 248

QY 82 AlaProProTyrglnGluLysArgValAlaLeuLeuMetAlaAlaLeuPheGlu 101

Db 249 ACTCTCTTATCAAGAGCAAAAGGTTGGCACTTCTGATGGCAGCTGCACTCTTTGAA 308

QY 102 GlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleValPhe 121

Db 309 GCGCTTCAATGGTGGCTTCTGATTGAATGGGCATCAACTTCGACCCCAAGCATTTGGCTT 368

QY 122 GlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeuAla 141

Db 369 GGTGCTTTTGTAGGTGTGGTGGCTTTTGGTCTCTCAGCTGCTGCCAATGTGGCA 428

QY 142 ArgArgArgGluTyLeuTyLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeuPhe 161

Db 429 AGGCGCAGGAGTACTTGTACCTTGGAGGCTTCTTTCATCTGGTGTCTCCCTCCTCATG 488

QY 162 TrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheIlePheGluLeu 181

Db 489 TGGTTCACATTGCACTCTCATCTTCTTGGTGGTGGCTTGGCTTTCAGATTTGAGGT 548

QY 182 TyrPheGlyLeuLeuValPheValGlyTyrlleValPheAspThrGlnGluIleIleGlu 201

Db 549 TATTTGGTCTCTTGGTCTTGGTGGCTACATAGTCTTTTGACCCCAAGAAATCATTTGAG 608

QY 202 LysAlaHisLeuGlyAspMetAspTyrrValLysHisAlaLeuThr 216

Db 609 AAGGTCACATTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 653

RESULT 3

CA811916

LOCUS CA811916 757 bp mRNA linear EST 11-APR-2003

DEFINITION CDNA clone CA41LN031vBf_D08 5', mRNA sequence.

ACCESSION CA811916

VERSION CA811916.1 GI:36260853

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

AUTHORS 1 (bases 1 to 757)

Goes da Silva, F., Lim, H., Iandolino, A., Baek, J., Jones, K., Walker M.A. and Cook, D.R.

TITLE Transcriptional responses of Vitis vinifera to infection by the bacterial pathogen Xylella fastidiosa

JOURNAL unpublished

COMMENT Contact: Doug Cook
CAES Genome Facility
UC Davis Department of Plant Pathology
1 Shields Ave., Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcocok@ucdavis.edu
Seq primer: GTTATCAGTCGACGGTACC.

FEATURES

Location/Qualifiers

1..757

Source

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="CA41LN031vBf_D08"

/sex="hermaphrodite"

/dev_stage="Late season sample"

/lab_host="DH5alpha"

/clone_lib="Cabernet Sauvignon Leaf - CA41LN"

/note="Organ: Leaf; Vector: pDNR; Site_: Sfil; Site_2: Sfil; CA41LN is a cDNA library of Cabernet Sauvignon leaves. The leaves were collected on September 20, 2001, in Napa Valley, California, and represent leaves in late season development. These leaves were asymptomatic and

were verified to be non-infected with the bacterial pathogen, *Xylella fastidiosa*, based on a diagnostic assay using PCR and *Xylella*-specific primer pairs. cDNA made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:

5'-AAGCAGTGTATCAACGAGAGTGGCATTCAGCGCGG-3' and 5'-ATTCAGAGCGGAGCGGCGCATATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

BASE COUNT 153 a 164 c 184 g 256 t
ORIGIN

Alignment Scores:

Pred. No.: 2,12e-88 Length: 757
Score: 1032.00 Matches: 196
Percent Similarity: 91.36% Conservative: 26
Best Local Similarity: 80.66% Mismatches: 20
Query Match: 81.13% Indels: 1
DB: 14 Gaps: 0

US-09-955-526-4 (1-248) x CA811916 (1-757)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTy 20

Db 29 ATGGAGGCGTTCCTGCGCTTTTTCGATTCAACAATCGAGCTCAAGGAGCGGTGGACCTAC 88

QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40

Db 89 GATTCACATCAAGAAATTCGCCGAGATTTCCTCGCGGTTCAAACATCTCTCAAGCAGGTT 148

QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrlleHisIleLeu 60

Db 149 TATCTCTCCCTGTGTGTGCTTGGTTCATCTGTCGAGGAGCTTACCTGCATCTTCTC 208

QY 61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80

Db 209 TGGAAATATGGTGGCTTCTTACTACTTTTGCANGCTTTGGAAGCATCATGATGGCTACTC 268

QY 81 SerAlaProProTyrglnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100

Db 269 TCTGCACCTTCATATGAAGAGAAAGAGGTTTCTACTATTCATGCGCTGTGGCCCTTTT 328

QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120

Db 329 CAAGGAGCCTCTATCGGTCCTTTGATTGACTTGGCTATTGAAATTCAGCCCAAGCATTCCT 388

QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeu 140

Db 389 GTTAGTGGCTTTTGGGGAACCTGCAGTGGCCCTTGGCTGTTTCTCGCGGCTGCAATGTG 448

QY 141 AlaArgArgGluTyLeuTyLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160

Db 449 GCAAGGCGCAGAGAGTACTTGTACTTGGAGGGGTCTTCTCTCTGGGCTCTCCATCCTT 508

QY 161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheIlePheGlu 180

Db 509 TCTGGTTCACATTGCTCTCTGCTGTTTGGGGGATCCACTGCCATCTTAAAGTTTGGAG 568

QY 181 LeuTyrrPheGlyLeuLeuValPheValGlyTyrlleValPheAspThrGlnGluIleLeu 200

Db 569 TTGTATTGTGACACTGTGTGGTGTGTGGGCTTACATGTAGTAGACACCCAGGACATATA 628

QY 201 GluLysAlaHisLeuGlyAspMetAspTyrrValLysHisAlaLeuThrLeuPheThrAsp 220

Db 629 GAGAAAGCCCATCTCGGGGATCGGAGTATGTGAACATCTCTCTCTCTCTCTCTCTCTCT 688

QY 221 PheGlyAlaValPheValArgIle-LeuIleIleMetLeuLysAsnAlaSerGluLysG 240

Db 689 TTTCTGCTGAGTTTGTTCGAATCCCTGATTCATGTTTGAAGAACTCGGCTGAAAGAG 748

QY 240 uGluLys 242

Db 749 TGAAGAG 755


```

RESULT 4
A1779122
LOCUS
DEFINITION
  ESN260001 tomato susceptible, Cornell Lycopersicon esculentum cDNA
  clone cLES7M13, mRNA sequence.
ACCESSION
  A1779122
VERSION
  A1779122.1 GI:5277163
KEYWORDS
  EST.
SOURCE
  Lycopersicon esculentum (tomato)
ORGANISM
  Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 596)
D'Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman
C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,
Giovannoni, J.J., and Martin, G.B.
Generation of ESTs from Pseudomonas susceptible tomato
Unpublished
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
  source
    Location/Qualifiers
      1..596
        /organism="Lycopersicon esculentum"
        /mol_type="mRNA"
        /cultivar="R11-13 (Rio Grande x Money Maker)"
        /db_xref="taxon:4081"
        /clone="cLES7M13"
        /tissue_type="leaf"
        /dev_stage="4-week old"
        /lab_host="SOLR"
        /clone_lib="tomato susceptible, Cornell"
        /note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLES - Tomato Pseudomonas Susceptible EST Library.
Directionally cloned cDNAs inserted into pBluescript SK(-)
at 5' end with EcoRI and 3' end with XhoI site"
BASE COUNT
  102 a 140 c 150 g 204 t
ORIGIN
Alignment Scores:
  2.36e-87 Length: 596
  1020.00 Matches: 198
  Percent Similarity: 100.00% Conservative: 0
  Best Local Similarity: 100.00% Mismatches: 0
  Query Match: 80.19% Indels: 0
  DB: 9 Gaps: 0
US-09-955-526-4 (1-248) x A1779122 (1-596)
QY 26 PheArgGlnIleSerProLeuValGlnThrHisLeuTyrLeuThrLeuCys 45
Db 2 TTCGCCAGATCTCACCTCTGTTCAAACTCATCTCAAGCAGGTGACCTTACGCTATGC 61
QY 46 CysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsnIleGlyGly 65
Db 62 TGTGCTTTAGTGGCATCGCTGCTGGGCTTACCTTCACATCTCTATGCAATATCGTGGC 121
QY 66 LeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProTyr 85
Db 122 CTCCTCACAAACAATGGCTGTGATGGGAAGCATGGTGGCTCTCTCTCAGCCTCTTAT 181
QY 86 GlnGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPheGlnGlyAlaSerIle 105
Db 182 CAAGAGCAAAAGAAGGTGGCTCTTCTGATGGCAGCTGCATTTTGAAGGCGCTCTATT 241
QY 106 GlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleValPheGlyAlaPheVal 125

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Db 242 GGTCTCTGATTGAGCTGGGCATTAACTTCGATCAAGCATTTGTCTTGGCGCTTTTGA 301
QY 126 GlyCysAlaValPheGlyCysPheSerAlaAlaMetLeuAlaArgArgGlu 145
Db 302 GTTTGTCTGTGGTTTGTGTTGCTTCTACGCTCTGCCATGTTGGCAAGCGCAGGAG 361
QY 146 TyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeuPheTrpLeuHisPhe 165
Db 362 TACTTGTACCTCGGGGGCTTCTTTCATCTCGCGCTCTCCCTTCTCTCTGTTGCATTT 421
QY 166 AlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGluLeuTyrPheGlyLeu 185
Db 422 GCATCCCTCCATTTTGGTGGTTCATGGCTGTTTCAAGTTTGAGTTGATTTTGGACTC 481
QY 186 LeuValPheValGlyTyrIleValPheAspThrGlnGluIleIleGluLysAlaHisLeu 205
Db 482 TTGCTGTTTGGGCTACATGCTCTTTGACACCCCAAGAAATTAATGAGAGGCTCATTG 541
QY 206 GlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAla 223
Db 542 GGTGATATGGATTACGTTAAGCATGTCATGACCTTTTCACAGATTTTGGCGCT 595
RESULT 5
BU023368
LOCUS
DEFINITION
  QHF10M17.yg.ab1 QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA
  clone QHF10M17, mRNA sequence.
ACCESSION
  BU023368
KEYWORDS
  BU023368.1 GI:22458888
SOURCE
  EST.
  Helianthus annuus (common sunflower)
  Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
1 (bases 1 to 732)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
singleton, see http://cgdb.ucdavis.edu/ for details.
Plate: QHF10 row: M column: 17.
FEATURES
  Location/Qualifiers
    1..732
      /organism="Helianthus annuus"
      /mol_type="mRNA"
      /cultivar="RHA280"
      /db_xref="taxon:4232"
      /clone="QHF10M17"
      /lab_host="E.coli"
      /note="vector: pBRCNAsFlab; The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB=QH_EFGHJ sunflower RHA280
TAG_TISSUE=hulls

```

```

BASE COUNT      159 a 171 c 154 g 248 t
ORIGIN
Alignment Scores:
Pred. No.:      6.89e-87      Length:      732
Score:          1016.00      Matches:      194
Percent Similarity: 92.67%      Conservative: 21
Best Local Similarity: 83.62%      Mismatches:   15
Query Match:     79.87%      Indels:       2
DB:              13      Gaps:       1

US-09-955-526-4 (1-248) x BU023368 (1-732)
QY 1 MetGluGlyPheThrSerPheAsp-----SerGlnSerAlaSerArgAsnArgTrrp 18
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 36 ATGGATTTCATCTCATCGTCTTCGATTCACATCGCATCGCTTCGTACACAGCTGG 95

QY 19 SerTyrAspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLys 38
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 96 ACTTACGATTCTCTCAAGAAATTTCCGTCAGATTCTCCCGTTGTCATCTCATCTCAA 155

QY 39 GlnValTyrLeuThrLeuCysCysAlaLeuValAlaSerAlaLaglyAlaTyrLeuHis 58
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 156 CAGGTTTAUCTGACACTATGTCGCGCTAGTAGCATCAGCCGTGGGGGCTTATCTTCAC 215

QY 59 IleLeuTrpAsnIleGlyLeuLeuThrMetAlaCysMetGlySerMetValTrrp 78
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 216 ATTCATTGGAACATTGGAGGCTCTTTGACACACCTTTGCAACCATAGATGCACTGTGG 275

QY 79 LeuLeuSerAlaProProTyrGlnGlnGlnLysArgValAlaLeuLeuMetAlaAla 98
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 276 TTAATCGCACTCTCCATATGAGAGCAAAAGGGTTTCACTATTGATGTCATCATCC 335

QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 336 CTCTTCCAGGACCTCTATGTCGCTTAATCGCTTAATCGCTGACCATGACTTTGACCCCAAGC 395

QY 119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAla 138
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 396 ATTTAGTAGAGCGCTGCTGGGACCGCCATGCTTCGCCCTTCCTTCAGGAGCTGCC 455

QY 139 MetLeuAlaArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSer 158
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 456 ATGTTGGCAGAGAGTAGAGAGTAATCTTATCTAGSAGGCTTCTGCTTCTGCTGTTCT 515

QY 159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys 178
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 516 ATACTCTCTGTTGTCATTTGCTTCATCCATCTTTGTTGTTCTATGCTATGTTCCAG 575

QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 576 TTGAGCTGATTTTGGGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 635

QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe 218
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 636 ATCATCGAAAGAGCTCATCTTGAGACTTGGATTATGTCAAGCATGCACTCACTCTTT 695

QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIle 230
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 696 ACCGACTTCGGTCTCTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 731

RESULT 6
CB978248
LOCUS
DEFINITION
cDNA clone CAB40005_IVa_Fa_C11 Cabernet Sauvignon Berry - CAB4 Vitis vinifera
ACCESSION
CB978248
VERSION
CB978248.1
KEYWORDS
GI:30301454
SOURCE
Vitis vinifera
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 : Vitaceae; Vitis
 1 (bases 1 to 706)
 Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Jones,K. and Cook
 ,D.
 Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
 berries at various developmental stages
 Unpublished
 Contact: Douglas Cook, PhD
 CAES Genome Facility
 UC Davis, Plant Pathology
 One Shields Ave., Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: drcook@ucdavis.edu
 Seq primer: ACGTACCGGACATATGCC.
 Location/Qualifiers
 1..706
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="CAB40005_IVa_Fa_C11"
 /sex="Hermaphrodite"
 /dev_stage="Berry on stage II, 9 mm"
 /lab_host="DH5alpha"
 /clone_lib="Cabernet Sauvignon Berry - CAB4"
 /note="Organ: Berry; Vector: pDONR; Site_1: Sfil; Site_2:
 Sfil; CAB4 is a cDNA library of Vitis vinifera cv.
 'Cabernet Sauvignon' Clone 8 berries. Sampled berries were
 collected from field-grown vines during stage II of berry
 growth (berries were green and hard) at approximately 60
 days after full bloom. The average berry size was 9
 millimeters. Sampled vines were located at the University
 of California, Davis, Experimental Vineyard. cDNAs were
 made by oligo-dT priming and directionally cloned. 5' and
 3' adaptors were used in cloning as follows:
 5'-AAGCATGTGTATCAAGCAGATGTCATTCAGCGCGG-3' and
 5'-ATTCTAGAGCCGCGGCGGACATG-dt(30)NN-3'. Library was
 constructed using the Clontech Creator SMART kit and
 size-selected to contain the 0.5-3 kb size fraction."

FEATURES

source

BASE COUNT 136 a 162 c 165 g 243 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.6e-86 Length: 706
 Score: 1012.00 Matches: 190
 Percent Similarity: 91.91% Conservative: 26
 Best Local Similarity: 80.85% Mismatches: 19
 Query Match: 79.56% Indels: 0
 DB: 14 Gaps: 0
 US-09-955-526-4 (1-248) x CB978248 (1-706)
 QY 4 PheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrrpSerTyrAspSerLeu 23
 |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
 Db 1 TTCTCTACGTTTTCGATTCACATCGATCGATCGGCGGTGGACCTACGATTCTC 60
 QY 24 LysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeuThr 43
 |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
 Db 61 AAGAAATTCGGCCAGATTTCTCTCGCTTCAACATCATCTCAAGCAGGTTTATCTCTCC 120
 QY 44 LeuCysCysAlaLeuValAlaSerAlaLaglyAlaTyrLeuHisIleLeuTrpAsnIle 63
 |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
 Db 121 CTGTGCTGTGCTTGTATTCATCTGTCGAGAGCTTACTGCTGCTGCTGCTGCTGCTGCT 180
 QY 64 GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrrpLeuLeuSerAlaPro 83
 |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
 Db 181 GGTGGCTTCTTACTACTTTTTCATGCTTTTGGAGCATCATATGCTACTCTCTGACCT 240
 QY 84 ProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPheGluGlyAla 103
 |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
 Db 241 TCATATGAAGAGAAAAGAGGTTTCACTATTGATGGCTGTGCGCCCTTTTCAAGAGGCC 300

```

QY 104 SerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleValPheGlyAla 123
DB 301 TCTATCGGCTCTTGAATGATTCGTGCTATTGAAATGACCAAGCATTCCTTTGATGCT 360
QY 124 PheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeuAlaArgArg 143
DB 361 TTTGTGGGAACGTCAGTGGCTTTGGCTGTTCTCTGCGGCTGCAATGTTGCAAGGCGC 420
QY 144 ArgGluTyrLeuTyrLeuGlyCysLeuLeuSerSerGlyValSerLeuLeuPheTyrLeu 163
DB 421 AGAGAGTACCTGTACTTGGGAGGGTCTTTCCTCTGGCCCTCCATCCCTTTCTGGGTG 480
QY 164 HisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGluLeuTyrPhe 183
DB 481 CACITTTGGCTCTCGTGTGTTGGGGGATCCACTGCCATCTTATGTTGAGTTGATTTT 540
QY 184 GlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleGluLysAla 203
DB 541 GCACTGTTGGTGTGTTGGGCTACATGTGTAGACACCCAGGACATAATAGAGAAAGCC 600
QY 204 HisLeuGlyAspMetAspTyrValIleHisAlaLeuThrLeuPheThrAspPheGlyAla 223
DB 601 CATCTCGGGGATCGGGACTGTGAACATCTCTCCCTTTTACATGATTTTGTCTGCA 660
QY 224 ValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu 238
DB 661 GTTTTGTTCGAATCCTCATTCATCATGTTGAAGAACTCGGCTGAA 705

RESULT 7
BU995008 739 bp mRNA linear EST 17-OCT-2002
LOCUS X018A11 Populus wood cDNA library Populus tremula x Populus
DEFINITION tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION BU995008
VERSION BU995008.1 GI:24106073
KEYWORDS EST.
ORGANISM Populus tremula x Populus tremuloides
SOURCE Populus tremula x Populus tremuloides
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosoids I; Malpighiales; Salicaceae; Populus.
REFERENCE 1 (bases 1 to 739)
AUTHORS Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
TITLE The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
JOURNAL Unpublished
COMMENT Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
source
1..739
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="wood"
/clone_lib="Populus wood cDNA library"

BASE COUNT 150 a 179 c 166 g 244 t
ORIGIN

Alignment Scores:
Pred. No.: 2,09e-84 Length: 739
Score: 990.00 Matches: 190
Percent Similarity: 89.18% Conservative: 16
Best Local Similarity: 82.25% Mismatches: 25
Query Match: 77.83% Indels: 0
DB: 13 Gaps: 0

US-09-955-526-4 (1-248) x BU995008 (1-739)

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QY 1 MetGluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTyrSerTyr 20
DB 46 ATGACGGCTTCGCTTCCTCTTTGACCTCAATCGGCTTCAACGAACGTTGGAGCTAC 105
QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
DB 106 GATTCTCTCAAGAACTTACGCCAGATCTCTCTCTGTCCAGAACCACTCTCAAGCAGTT 165
QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
DB 166 CATCTGACCTTATGTGTGCACTGGTTCATCTCCGCTGGGGCATACCTCCATATTCTG 225
QY 61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTyrLeuLeu 80
DB 226 TGGATATGTGTGCTCTTAAACGACATCCCAAGCTTTGGATGATGATGCTTGGCTACTT 285
QY 81 SerAlaProProTyrGlnGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
DB 286 TCCATATCTCCTTATGAAGACAAAGAGGGTGGTCTCTCTTATGGCAACGCACTCTTC 345
QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
DB 346 CAAGGGGCTCTATAGGTCCTCTGATGATCTGGCCATTCAGATGATCCCAAGTGTCTG 405
QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeu 140
DB 406 ATTACAGCTTTTGTGGGAACTCGGGTAGCTTTGGATGTTCTCAGTAGCAGTATGTTG 465
QY 141 AlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
DB 466 GCTAGCGCTAGAGAATATCTTTACTTGGTGGCTTGTCTTCATCGGCTTTCCATCCTT 525
QY 161 PheTyrLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180
DB 526 CTATGGCTGCATTTGCATCTCCATCTTGGGGATCTGGAGCCTCTTAAATTTGAG 585
QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleLeu 200
DB 586 CTGTACTTTGGGCTCTCTGGTGTGTGGGCTATGTGTAGTGTGACACCCAGGATATCAT 645
QY 201 GluLysAlaHisLeuGlyAspMetAspTyrValIleHisAlaLeuThrLeuPheThrAsp 220
DB 646 GAGAAAGCTCCTCTGGTGTGATCTGGGATGGAAGCATTCCTCGAGCTTTTCACAGAC 705
QY 221 PheGlyAlaValPheValArgIleLeuIleLeu 231
DB 706 TTCGTTGCTGTTTTCGGAATTCCTCAATC 738

RESULT 8
BU933489 671 bp mRNA linear EST 18-OCT-2001
LOCUS EST553378 tomato flower, anthesis Lycopersicon esculentum cDNA
DEFINITION clone cTOD16N14 5' end, mRNA sequence.
ACCESSION BU933489
VERSION BU933489.1 GI:16247961
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 671)
AUTHORS van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
Utterback, T., Van Aken, S., Ronning, C.M., Niernan, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
TITLE Generation of ESTs from tomato flower tissue, anthesis (2001)
JOURNAL Unpublished
COMMENT Contact: CUGI
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html

```

This clone is available through the Clemson University Genomics Institute
 Seq primer: r3.
 Location/Qualifiers

FEATURES

Source
 1..671
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cT0016N14"
 /tissue_type="flower"
 /dev_stage="anthesis"
 /clone_lib="tomato flower, anthesis"
 /note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

BASE COUNT
 134 a 161 c 157 g 219 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1..11e-81 Length: 671
 Score: 961.00 Matches: 196
 Percent Similarity: 98.49% Conservative: 0
 Best Local Similarity: 98.49% Mismatches: 3
 Query Match: 75.55% Indels: 2
 DB: 12 Gaps: 0

US-09-955-526-4 (1-248) x BI933489 (1-671)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
 Db |||||
 76 ATGGAAGGTTTCACATCGTTCTCGACTCGCAATCGCTCTCGCAACGCTGGAGTTAT 135
 QY 21 AspSerLeuLysAspPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
 Db |||||
 136 GATTCTCTCAAAACCTTCGCCAGATCTCACCTCGTTTCAAACTCATCTCAAGCAGGTTG 195
 QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
 Db |||||
 196 TACCTTACGCTATGCTGTGCTTTAGTGGCATCGCTCGCTGGGGCTTACCTTCACATTCFA 255
 QY 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
 Db |||||
 256 TGGAAATATCGTGGCTCTCTCAACAATGGCTTGCATGGGAAGCATGGTGGCTTCFC 315
 QY 81 SerAlaProProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
 Db |||||
 316 TCAGCTCTCCCTATCAAGAGCAAAAGGGTGGCTCTTCTGATGGCAGCTGCACCTTTT 375
 QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPhaAspProSerIleVal 120
 Db |||||
 376 GAAGCGCTCTATTTGGTCTCTGATTGAGCTGGGCATTAATTCGATCCAGCATTTGG 435
 QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeu 140
 Db |||||
 436 TTTGGCGCTTTTGTAGTTGTCTGTGGTTTTTGGTTGCTTCTCAGCTCTGCCATGTTG 495
 QY 141 AlaArgArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
 Db |||||
 496 GCAAGCGCAGGAGTACTTTGACCTCGGGGGCCCTTCTTTCATCTGGCGTCTCCCTTCFC 555
 QY 161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180
 Db |||||
 556 TTCTGGTTCACCTTTCGATCTCTCATTTTGTGTGTTCCATGGCTGTTTCAAGTT-GAG 613
 QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluLe 199
 Db |||||
 614 TTGTATTTGGACTCTTGGTGGTTTGTGGGCTACATCGTCTTTGACACCCCAAGAAATT 670

RESULT 9

FEATURES

Source
 1..643
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="Rio Grande PtoR"
 /db_xref="taxon:4081"
 /clone="cLET39W7"
 /tissue_type="leaf"
 /dev_stage="4-6 week old plants"
 /lab_host="XLI-Blue MRP"
 /clone_lib="tomato mixed elicitor, BTI"
 /note="Vector: pBlueScript SK(-); Site.1: EcoRI; Site.2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, Erix, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

BASE COUNT
 129 a 155 c 150 g 209 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1..32e-81 Length: 643
 Score: 960.00 Matches: 186
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 75.47% Indels: 0
 DB: 9 Gaps: 0

US-09-955-526-4 (1-248) x AW096641 (1-643)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
 Db |||||
 85 ATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCGCTCTCGCAACGCTGGAGTTAT 144
 QY 21 AspSerLeuLysAspPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
 Db |||||
 145 GATTCTCTCAAAACCTTCGCCAGATCTCACCTCGTTTCAAACTCATCTCAAGCAGGTTG 204
 QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
 Db |||||
 205 TACCTTACGCTATGCTGTGCTTTAGTGGCATCGCTCGCTGGGGCTTACCTTCACATTCFA 264
 QY 61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
 Db |||||
 265 TGGAAATATCGTGGCTCTCTCAACAATGGCTTGCATGGGAAGCATGGTGGCTTCFC 324
 QY 81 SerAlaProProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
 Db |||||

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Db      325 TCAGCTCCTCTTATCAAGACAAAAAGGGTGGCTCTTCTGATGGCAGCTGCACCTTTT 384
Qy      101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
Db      385 GAAGCGCCTCTATGGCCCTCTGATGAGCTGGCACTTAACCTCGATCCAGCATTTGG 444
Qy      121 PheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaAlaMetLeu 140
Db      445 TTTGGCGCTTTGTAGGTGTGCTGTGTTTGGTCTCTCAGCTGCTGCCATGTTG 504
Qy      141 AlaArgArgGluTyTyLeuTyTyLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
Db      505 GCAAGCGCAGGAGTACTTACCTCGGGGCCCTCTTCTCATCTGGCGTCTCCCTTCTC 564
Qy      161 PheTyrPheLeuHspheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180
Db      565 TTCGTGGTGCACCTTTCATCTCCATCTTTTGGTGTTCATCGGCTGTTTCAAGTTTGA 624
Qy      181 LeuTyTyPheGlyLeuLeu 186
Db      625 TTGTATTTGGACTCTTG 642

RESULT 10
AW219279
LOCUS   AW219279
DEFINITION EST301761 tomato root during/after fruit set, Cornell University
Lycopersicon esculentum cDNA clone cLEX3N8, mRNA sequence.
ACCESSION AW219279.1 GI:6530153
VERSION   1
KEYWORDS  EST.
SOURCE    Lycopersicon esculentum (tomato)
ORGANISM  Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 646)
AUTHORS   van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Renning,C.M.,
Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato root tissue
Unpublished
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES             source
     1..646
     /organism="Lycopersicon esculentum"
     /mol_type="mRNA"
     /cultivar="TA496"
     /db_xref="taxon:4081"
     /clone="cLEX3N8"
     /tissue_type="root"
     /dev_stage="plants during and after fruit-set"
     /clone_lib="tomato root during/after fruit set, Cornell
University"
     /note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin
(USDA-ARS, Ithaca, NY 14850)."
```

BASE COUNT 131 a 155 c 151 g 209 t

ORIGIN

Alignment Scores:

Pred. No.: 2,31e-80 Length: 646
Score: 947.00 Matches: 186
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 0
Query Match: 74.45% Indels: 1
DB: 9 Gaps: 0

US-09-955-526-4 (1-248) x AW219279 (1-646)

```

Qy      1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTyrSerTyr 20
Db      87 ATGAAGGTTTCACATCGTTCTTCGACTCGCAATCGCTCTCGCAACCGCTGGAGTTAT 146
Qy      21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
Db      147 GATTCTCTCAAAAACTTCGGCCAGATCTCACTCTCGTTCAAACTCACTCAAGCAGGTG 206
Qy      41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyTyLeuHisLeuLeu 60
Db      207 TACCTTAGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGCTTACCTTCACATTCTA 266
Qy      61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db      267 TGGAAATATCGTGGCTCTCTCACAAATGCTTGCATGGGAAGCATGGTGGGTTCTC 326
Qy      81 SerAlaProProTyTyGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
Db      327 TCAGCTCCTCTTATCAAGAGCAAAAAAGGGTGGCTCTTCTGATGGCAGCTGCACCTTTT 386
Qy      101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
Db      387 GAAGCGCCTCTATTTGGTCTCTGATTGAGCTGGGCACTTAACCTCGATCCAGCATTTGG 446
Qy      121 PheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaAlaMetLeu 140
Db      447 TTTGGCGCTTTTGTAGGTGTGCTGTGTTTGGTGTTCATCGCTGCCATGTTG 506
Qy      141 AlaArgArgGluTyTyLeuTyTyLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
Db      507 GCAAGCGCAGGAGTACTTGTACCTCGGGGCCCTCTTCTCATCTGGCGTCTCCCTTCTC 566
Qy      161 PheTyrPheGlySerIlePheGlyGlySerMetAlaValPhe-LysPheGly 180
Db      567 TTCGTGGTGCACCTTTCATCTCCATTTTGGTGTTCATCGCTGTTTCAAACTTGA 626
Qy      180 uLeuTyTyPheGlyLeuLeu 186
Db      627 GTGTATTTGGACTCTTG 645

RESULT 11
BG839316 831 bp mRNA linear EST 25-MAY-2001
Gm01_16b10_A Gm01_AAFEC_ECORC_Glycine_max_cold_stressed_leaves
Glycine max cDNA clone Gm01_16b10, mRNA sequence.
ACCESSION BG839316
VERSION   1
KEYWORDS  EST.
SOURCE    Glycine max (soybean)
ORGANISM  Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 831)
AUTHORS   Singh,J.A., Robert,L.S., Lu,B., Zhu,L., De Moors,A., Couroux,P.,
Harris,L.J., Hattori,J.I., Ouellet,T., Spratt,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Glycine max (soybean)
Leaves
Unpublished
Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neathy Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
FEATURES             Location/Qualifiers
     1..831
     /organism="Glycine max"
     /mol_type="mRNA"
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```
/cultivar="Maple Arrow"  
/db_xref="taxon:3847"  
/clone="Gm01_18b10"  
/tissue_type="Leaves"  
/dev_stage="15-day seedlings"  
/clone_lib="Gm01_AAF_C_ECORC_Glycine_max_cold_stressed_leaves"
```

/notes=Vector: Bluescript SK-/XhoI-EcoRI; Site_1: EcoRI; Site_2: XhoI; Plants were grown 12 days from seeds, treated at 20C for 3 days, then leaves were collected. Library was prepared using Unizap ZAP-cDNA synthesis kit / Packaged GigaPack III Gold." 207 c 158 g 3 others

BASE COUNT	298 a	207 c	158 g	165 t	3 others
BASE COUNT	298 a	207 c	158 g	165 t	3 others

Alignment Scores:	
Pred. No.:	1.36e-79
Score:	940.00
Percent Similarity:	79.54%
Best Local Similarity:	74.06%
Query Match:	73.90%
DB:	12
Length:	83
Matches:	177
Conservative:	37
Mismatches:	25
Indels:	1
Gaps:	0

US-09-955-526-4 (1-248) x BG839316 (1-831)

QY 10 SerGlnSerAlaSerArgAsnArgTrpSerTyrAspSerLeuLysAsnPheArgGlnIle 29
 ||| : : : : : : : : : : : : : : : :
Db 831 TCCTCTCTCTCGAGAAGCCGGTGGACTACGATACCTCAGAATAATTCGTGAGATC 772

30 SerProLeuValGlnThrHisLeuLysGlnValTyrLeuThrLeuCysCysAlaLeuVal 49
|||||
771 TCTCGGTGTTCAAGATCAATCAACACGGGTTTATTTACGTTATGTTGGCTGTGGTG 712

50 AlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsnIleGlyGlyLeuLeuThr 69
 |||||
 711 GCGTGTGTGGAGCTTCTTCATGTTCTCTGGAACATTGGGGTTTCTTCACAG 652
 |||||

70 MetaLaCySMetGlySerMetValTrpLeuLeuSerAlaProPrtYrGlnGluGlnLys 89
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
651 TTGGTTCCTCCATTGAAGCATCGTTGTG-TTGCTATCTACACCCCTCTTGTAAGAGCAAAAG 593

QY	90	ArgValAlaLeuLeuMetAlaAlaAlaLeuPheGluGlyAlaSerIleGlyProLeuIle	109
Db	592	AGGTGTCTGTGTGATGGCTTCGGCCCTCTTTTCAGGGCGCTTCCATTGGACCTCTGATT	533

QY 110 GluLeuGlyIleAsnPheAseProSerIleValPheGlyAlaPheValGlyCysAlaVal 129
 ::::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 532 GATTGGCATATGCCATTGATCTAGCGTTATTGTATTAGTCATTCTGGCAACTCTTGG 473

QY 130 ValPheGlyCysPheSerAlaAlaAlaMetLeuAlaArgGArgGluTyrLeuTyrLeu 149
 472 GCTTTTGCTTCTCTCTGGGAGCTTTAGTTGCAAGCGTAGAGAGTACCTACACCT 413
 Db

150 GlyGlyLeuLeuSerSerGlyValSerLeuLeuPheTrpLeuHisPheAlaSerSerIle 169
 412 GGTGGTTCGTCCTCTCGGCTCCATCTCTATGCTGGTGCATTGTGCTCTCTCTC 153

QY	170	PheGlyGlySerMetalavalPheLysPheGluLeuTyPheGlyIleuValPheVal	189
Db	352	TTTTGGGGCTCAATTGCACCTTCAAGTTTGAGCTACTTTGGCGCTTTGTGTTTTC	393

QY 190 GlyTyrIleValPheAspThrGlnGluIleLeuGluLysAlaHisIleuGlyAspMetAsp 209
292 GSCTACGTCATAGTAGACATCTCACAAATTTATTCACAAAGCGCTCATCGTTTCGACGACG 232
Db 292 GSCTACGTCATAGTAGACATCTCACAAATTTATTCACAAAGCGCTCATCGTTTCGACGACG 232

[illegible][illegible]

172 **ATTAATATGTTGAGAGCAATTCACTGAGAGAAATGAGAAGAAGAAAAAGGAGAGAT** 116

RESULT 12	
BQ856331	
LOCUS	
DEFINITION	

DEFINITION	ACCESSION
	VERSION
	KEYWORDS
	SOURCE
	ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

FEATURES SOURCE

[illegible]

Alignment Score:
Pred. No.:
Score:

Percent Sim
Best Local
Query Match
DB:

US-09-955-55

QY Db

Qy	1
Db	1

BQ856331 723 bp mRNA linear EST 14-AUG-2002
 QGB2h05.yg.ab1 OG_ABCDI lettuce salinas lactuca sativa cDNA clone
 QGB2h05. mRNA sequence.
 BQ856331
 BQ856331.1 GI:22241796
 EST.
 Lactuca sativa
 Lactuca sativa
 Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
 Cichoraceae; Lactuca.
 1 (bases 1 to 723)
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
 P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
 Church, S., Jackson, L. and Bradford, K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://comgenomics.ucdavis.edu/>
 Unpublished
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel.: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@atgc.org [michelmore@vegmil.ucdavis.edu]
 belongs to contig QG_CA_Contig7943, see <http://cgdb.ucdavis.edu/>
 for details.
 Plate: QGB2 row: h column: 05.

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1. 723
Location/Qualifiers
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QGB2h05"
/lab_host="E.coli"
/clone_lib="QG-ABCD1 lettuce salinas"
/note="Vector: pBRCNDNASFIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_Lib-QG-ABCD1 lettuce salinas
TAG_TISSUE=leaves dark grow

```

159 a	174 c	141 g	249 t	
TAG_SEQ=GCTAGTCGGG"				
cores:				
	5.55e-79	Length:	723	
	933.00	Matches:	180	
ilarity:	89.23%	Conservative:	20	
Similarity:	80.36%	Mismatches:	21	
	73.35%	Indels:	3	
	13	Gaps:	1	

26-4 (1-248) x BQ856331 (1-723)

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1 1 MetGluGlyPheThrSerPheAspSerGln-----SerAlaSerArgAsnArgTyr 18
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
20 ATGGAATCATCTCATCTGCTTCCTGCATTCACAAATCGGATCGCTTCTCCAAACACCTCG 109
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
9 9 SerTyrAspSerLeuLyAsnPheArgGlnIleSerProLeuValGlnThrIleLeuLys 38
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
10 ACCATCAGATCTCTCAAGAAATTCGGTCAAACTCTTCCTTATGTTACAGACTCATCTCAA 169
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
```

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Qy 39 GlnValTyrLeuThrLeuCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHis 58
Db 170 CAGTTTACCTCTCAGTATGCTGCTCATGCGATCGAGTTGGGGCTTACCTTCA 229
Qy 59 IleLeuTrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrp 78
Db 230 ATCTATGAACATCGGTGGCTTCTAACACCTTCGGAACGTTGGGCTGCATGTTTGG 289

Qy 79 LeuLeuSerAlaProTyrGlnGluGln-LysArgValAlaLeuLeuMetAlaAla 98
Db 290 CTATCGCCACTCCACAAATATCAAGACAAAAGAGTCTCTATTAATGGCATCTTC 349
Qy 98 aLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProse 118
Db 350 TCTTCTCCAGGACCTCCATCGGTCTCTAATCGACTTAGCCCATAGAAATTGACCCAA 409

Qy 118 rIleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAla 138
Db 410 CATCTTGGTGAGCGGTTTCATGGGAAGTCAATCGCATTTGCTTGTTCAGGAGCTGC 469
Qy 138 aMetLeuAlaArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSe 158
Db 470 CATGTTAGACAGCGAGAGTATCTTATCTTGGAGGCTCTCTTCTTCTGTGTTC 529

Qy 158 rLeuLeuPheTrpLeuHisPheAlaSerIlePheGlyGlySerMetAlaValPheLy 178
Db 530 AATCCTTTCTGTTACATTTGCTCATCAATCTTTGGTGGCTCTGTGCTTTTCAA 589
Qy 178 sPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnG 198
Db 590 ATTTGAGTTGACATTTGGGCTGTTGGTGTGTTGGGTACATGGTGGTTGACCCCAAG 649
Qy 198 uIleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPh 218
Db 650 TATCATGAAAGGCTCATCTTGAGATTGGATTGATGTAACATGCTCTTACGCTTT 709

Qy 218 eThrAspPhe 221
Db 710 CACTGATTTTC 719

RESULT 13
BG127849
LOCUS
DEFINITION
EST473495 tomato shoot/meristem Lycopersicon esculentum cDNA clone
ctof18E8 5' sequence, mRNA sequence.
ACCESSION
BG127849
VERSION
BG127849.1 GI:12628037
KEYWORDS
EST.
SOURCE
Lycopersicon esculentum (tomato)
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 647)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
Unpublished
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1. 647
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="ctof18E8"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
FEATURES
source

```

```

/lab_host="SOLR"
/clone_lib="tomato shoot/meristem"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."

```

```

BASE COUNT      129 a   154 c   153 g   211 t
ORIGIN

Alignment Scores:
Pred. No.:      6.21e-79      Length:      647
Score:          932.00      Matches:      186
Percent Similarity: 98.41%      Conservative: 0
Best Local Similarity: 98.41%      Mismatches: 1
Query Match:      73.27%      Indels:      2
DB:              10          Gaps:      0

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US-09-955-526-4 (1-248) x BG127849 (1-647)

```

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Qy 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
Db 85 ATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCTCTCGCAACCGCTGGAGTTAT 144
Qy 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
Db 145 GATTCTCTCAAAACTTCCGCCAGATCTCACTCTCGTCAAACTCACTCAACAGAGTG 204
Qy 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
Db 205 TACCTTAGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGGCTTACCTTTCACATTCTA 264
Qy 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 265 TSGAATATCGGTGGCTCTCTCACAACTATGCTTCGATGGGAAGCTGGTGTGCTCTTC 324
Qy 81 SerAlaProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaAlaLeuPhe 100
Db 325 TCAGTCTCTCTTATCAAGACGCAAAAAGGGTGGCTCTTCGATGGGAGCTGCACCTTTT 384
Qy 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
Db 385 GAAGCGCGCTCTATTTGGTCTCTGATTGAGCTGGGCAATTAACATCGATCCAAGCATTTG 444
Qy 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeu 140
Db 445 TTTGGCGCTTTTGTAGGTGTGCTGTGTTTGGTGTCTTCTCAGCTGCTGCCATGTG 504
Qy 141 AlaArgArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeu 160
Db 505 GCAAGCGCAGGAGTACTGTACTCGGGGCGCTTCTTTCATCTGCGCTCTCCCTTCTC 564
Qy 161 PheTrpLeuHisPheAlaSerSerIlePhe-GlyGlySerMet-AlaValPheLysPheG 180
Db 565 TTCTGGTGGCACTTTGTCATCTCTTCAATTTTGGTGGTTCATGGGCTCTTTTCAAGTTTG 624
Qy 180 LuLeuTyrPheGlyLeuLeuVal 187
Db 625 AGTTGATTTTGGGACTCTTTGGG 647

```

```

RESULT 14
BU896719
LOCUS
DEFINITION
X044G02 Populus wood cDNA library Populus tremula x Populus
tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION
BU896719
VERSION
BU896719.1 GI:24107926
KEYWORDS
EST.
SOURCE
Populus tremula x Populus tremuloides
ORGANISM
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurossids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 691)

```


Db 409 ATTACAGCTTTGTGGGAACCTGGGTAGCTTTGGATGTTCTCAGTAGCAGCTATGTTG 468
QY 141 AlaAtgAgtArgGluTyrLeuTyrLeuGlyLeuSerSerGlyValSerLeuLeu 160
Db 469 GCCAGCGTAGAGAAATATCTTTACTTGGGTGGCTTGCTTTCATCTGGCCCTTTCCATCCTT 528
QY 161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180
Db 529 CTATGGCTGCACCTTTGCATCCTCCATCTTTGGGGATCTGCAGCCCTCTTTAAATTTGAG 588
QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIle 200
Db 589 CTGTACTTTGGGCTTCTGTGTGTTGTGGGTATGTGGTAGTTGCACACCCAGGATATCATT 648
QY 201 GluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeu 215
Db 649 GAGAAAGCTCACCTTGGTGTATCTGGACTATGTGAACCAATCCCTG 693

Search completed: September 22, 2003, 16:55:51
Job time : 2072 secs